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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AX036541 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		C 45	C 43		40	c. 38	ıω	с 35	w	c 31	ωı	22 29	NN	c 25	23	N N	c 20	18	<u>_</u>	a 15	ىر د	11 12	10	တထ	70) N N H	Result No.
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                                                                        Direct Submission
Direct Submission
Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
CAMBRIDGESHIRE, CB10 1SA, UK. CB10 1S
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 189967)
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Center: Wellcome Trust Sanger Institute
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/translation="EzereDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIV
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Insert size: 215919; 10.9% error; agarose-fp
Quality coverage: 5.28x in Q20 bases; sum-of-
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Consensus quality: 186623 bases at least Q40
Consensus quality: 187480 bases at least Q30
Consensus quality: 188086 bases at least Q20
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Contact: humquery@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently * consists of 13 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coverage: 4.68x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: bM17A4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130770 130869: gap of 100 bp
130870 146267: contig of 15398 bp in length
146268 146367: gap of 100 bp
146368 151984: contig of 5617 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151985 152084: gap of
152085 184112: cont
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122177 130769: contig of 8593
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184213 189967: contig of 5755
Location/Qualifiers
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8455 8554: gap of 100 bp

8555 19307: contig of 10753 bp in length

19308 19407: gap of 100 bp

19408 27097: contig of 7690 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27098 27197: gap of 100 bp
27198 40822: contig of 13625 bp in length
                                                                                                                         /note="assembly_fragment:00259
fragment_chain:1"
27198. .40822
                                                        40923.
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                          fragment_chain:1
clone_end:SP6
/note="assembly_fragment:00793
fragment_chain:2"
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fragment_chain:1"
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/chromosome="4"
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    Summary Statistics

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135;
                                           Direct Submission
Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: cloneequest@sanger.ac.uk
   Center:
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                             sequence.
AL807815
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ALBU/RID
ALBU/RID
ANA Linear ROD 22-AUG-2002
AUGUSE DNA sequence from clone RP23-207HI6 on chromosome 4, complete
                                                                                                                               Leongamornlert,D.
                                                                                                                                                                                                                                                            AL807815.3 GI:22474427
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                                23, 2002 this sequence version replaced gi:21690116
Wellcome Trust Sanger Institute
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/note="assembly_fragment:00178
fragment_chain:3
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fragment_chain:2"
95033..109692
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fragment_chain:3"
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fragment_chain:3"
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fragment_chain:2"
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fragment_chain:2"
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               Genome Center
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DEFINITION ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCA 336
                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                      Caenorhabditis elegans
1 (bases 1 to 40090)
                                                                                                              Caenorhabditis elegans.
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                                                                                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                                                                  AC006611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                            AC006611.1 GI:4263327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-207H16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones.
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/clone_lib="RPCI-23"
37887 c 37484 g 67430 t
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/db_xref="taxon:10090"
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                                                                                                                                                                                                    40090 bp DNA cosmid C30F8, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington Submission
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                                                                                                                                                                                                                                                                                    Submitted (12-FEB-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Latreil, P., Twyman, B. and Wilson, R. The sequence of C. elegans cosmid C30F8
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-OCT-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
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Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , Mo 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
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neighboring submissions. NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between

or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist: more than one m13 subclone. an alternate chemistry

CDS

For a graphical representation of this cosmid sequence and its {www.wormbase.org/db/seq/sequence?name=C30F8; class=Sequence}

NEIGHBORING COSMID INFORMATION

/codon_start=1 /product="Hypothetical protein C30F8.4a" /protein_id="AaK88457.1" /db_xref="GI:15150650"

/note="similar to protein kinases (PFam; pkinase, score; 183.25); coded for by the following C. elegans cDNAs: yk739d9.5, yk284c11.3, yk284c11.5, yk465a7.5, yk739d9.3, yk649h5.5"

The ω cosmid is 8300 bp overlap; the 3' cosmid is Y110A7A,

200 bp overlap. Actual start of this cosmid is at base position 197 of C30F8; actual end is at 40090 of C30F8.

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORPeome cloning project (http://worfdb.dfcl.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans researchers trNAs are predicted using the program tRNAscan SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964). Location/Qualifiers

FEATURES gene gene CDS misc_feature misc_feature source complement(21528. .21529)
/note="SL1 trans-splice site; see yk821a09.3"
complement(21534. .21535) /note="coded for by the following C. elegans cDNAs: yk710g2.3, yk449d2.3, yk705g11.3, yk745d7.3, yk165b6.3, yk809d10.3, yk805a04.3, yk702g3.3, yk105h9.3, yk105h9.5, yk169b6.5, yk306e11.3, yk306e11.5, yk431f1.3, yk431f1.5, yk449d2.5, yk479e6.5, yk859d05.5, yk710g2.5, yk702g3.5, yk449d2.5, yk479e6.5, yk859d05.5, yk72a09.5, yk805g31.5, yk763e04.5, yk82a09.5, yk809d10.5, yk773c05.5, yk705g11.5, yk754e11.5, yk807a04.5, yk82a09.3" complement(19565.
/gene="C30F8.2" join(25607. .25684,27245. .27344,27393. .27492,27665. .2 28346. .28436,28489. .28707,28818. .29897,29946. .30020, 30070. .30315,32038. .32325,32760. .32891) /gene="C30F8.4" /translation="MGEFLFNIDHGYLEALIRGLKGGLLAQADYANLYQCETLEDLKL HIQSTDYGTHQREISELLINKCHPUGSFBOMEAIHLASNTALEPLATFLDYITYSYM IDNIILLITGTHQREISELLINKCHPUGSFBOMEAIHLASNTALEYNAVLVDTPLANY FVDCINEQDLDEMNVEVIRNTLYKAYIEDFYKFCAGLGGKTAEVMCDILAFEADRRSI complement(join(19565..19654,20030..20101,20153..20407, 20460..20617,20879..21057,21102..21273,21392..21512)) /organism="Caenorhabditis elegans" /strain="Bristol N2" /db_xref="taxon:6239" IITINSFDTELSKDDRQKLYPRCGKLFPDGLTGLSRADDYDQVKQVCEFYSDYKPLFE GSGNGPGEKTLEDKFFEHEVKLNVHSYLHQFHFGVFYAFIKLKEQEMRNIIWIAECIS /product="Hypothetical protein C30F8.2"
/protein_id="AAK85455.2"
/db_xref="GI:16259229" QRHRTKIDNYIPIM" /codon_start=i /gene="C30F8.2" /note="for a graphical representation of this gene see: {www.wormbase.org/db/seq/sequence?name=C30F8.2;class=Seque /clone="C30F8" /chromosome="I" /gene="C30F8.4" note="SL1 trans-splice site; see yk809d10.5" www.wormbase.org/db/seq/sequence?name=C30F8.4a;class=Sequ 'note="for a graphical representation of this gene see: 3289 .21512) .27859

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RESULT 5
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/gene="C30F8.3"
/note="for a graphical representation of this gene see:
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ATIRFKTPNNIDSNIRLRRELITLKELIGGOFGNVYKAVYHDLEKDERIAVAVKVCK
TDAEFADTOLILQESSIMRNERHSNIIOLIGVCVDOPMMIVLEAPRGELREVILQOEK
DWLPLRILTLFCSQICDSLVYLHSTRFVHRDIAARNIILYCSPOCVKLADFGLSRALDY
DAVYTASRGKLPIKWLAPESVNIYROFSMASDVWMEGVCMWEIFSLGVKWAAGVTNSDV
IMHIEOGSRPPCPEKCPTALYNFIRSKMWAIEPHKRPTVDQIYAIIEDVRQQIIQNIP
PEQIIVGKPWTAAGVIVVAEMSSLPGLTLYRTWEDQKRQAEEDAKWLEQEDDEDEDQD
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GELREYLQQEKDWLPLRILTLECSQICDSLVYLLSTREVHRDIAARNILUCSPQCVXL
ADFGLSRALVYDAVYTASRGKLPIKWLAPESVVXLQESMASDVWMFGVCWMEIFSLGV
KPWAGVTNSDVIMHIEQGSRPPCPEKCCTALYNFIRSKWWAIEPHKRPYVDQIYAIIE
DVRQQIIQNIPPEQIIVGKPWTAAGVLYVAEMSSLPGLTLYRTMEDQKRQAEEDAKWLE
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SAFVTLHEQVVDEFFSHVANKSSVEVALEVAALKVCRDFAEHGHNKGADHHLEDLDIE
ACIOSLIPBVHUNPGFKHSHLKKTFTAYIKKESATSPNESIIRSLALLLEVVKEDVEL
FKASLGAGWTKPVELVVGPHTGLSYRLNERCDSSRLLELRTIAEITIRKMENGSEKTL
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RKMENGSEKTLMQLNLSGAAKPVLITLSTEELSQSLAHLLDGYQMLYNQRDSVFKLKG
IERCETLTMHEATIRPKTPNNIDSNIELRRELITLKELIGGGQFGNVYKAVYHDLEKD
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SFNNLTHNDDFLHSVKEVTSQLREMLIVASGMRDRVTTTTQRTDVDMTKTLIANDMKQ
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GVCDAVTKLQNSFNNLTHNDDFLHSVKEVTSQLREMLIVASGMRDRVTTTTQRTDVDM
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ADHHLEDLDIEACIQSLIPNVLHNPGFKHSHLKKTFTAYIKKFSATSPNESIIRSLAL
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/protein_id="AAM15554.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                    AC115614 4458 bp DNA linear HTG 21-MAR-2002 Dictyostelium discoideum chromosome 2 map 5179259-5183715 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                   Dictyostelium discoideum.
Dictyostelium discoideum
                                                                            HTG; HTGS_PHASE2.
                  Eukaryota; Mycetozoa;
                                                                                               AC115614.1 GI:19570143
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Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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  development
Patent: WO 9950284-A 5 07-OCT-1999;
Patent: WO 9950284-A 5 07-OCT-1999;
AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP
ANDREAS (DE); WIRTH THOMAS (DE)
                                                                                                                                                                                                                                                                                          Sequence 5 from Patent WO9950284. AX015902
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Aigner, T., Hess, J., R
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MOTE: This is a 'working draft' sequence.
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by the finished sequence as soon as it is available
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                                                           ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG 9377
                                                                                      AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49999 bp
Sequence 11 from Patent WO9950284.
AX015908
                                                                                                                                                                                                                                                                                                                                                                                        AIGNER THOMAS (DE); HESS JOCHEN (DE); ANDREAS (DE); WIRTH THOMAS (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 9950284-A 11 07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                    development
                                                                                                                                                                                                                                                                                                                                                                                                                                               Aigner,T., Hess,J., Rosenthal,A., Rump,A. a Nucleic acid molecules which code proteins
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1 (bases 1 to 49999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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/db_xref="taxon:10090"
a 11814 c 10825 g 14150 t
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                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
11787 c 10868 g 14209 t
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                                                                                                                                                                                                                                      Score 45.8; DB 6;
Pred. No. 0.33;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGCAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9120)
On Jul 10, 2002 this sequence warri-
                                                                                                                                                                                                                                                                             AF312994 228283 bp DNA linear ROD Mus musculus chromosome 1 clone MML, complete sequence. AF312994
      Submitted
                    Rump,A., Hess,J., Galgoczy,P., Wirth,T. and Rosenthal,A. Direct Submission
                                                                              Unpublished
                                                                                                1 (bases 1 to 228283)
Rump,A., Hess,J., Galgoczy,P., Wirth,T. and Rosenthal,A.
Genomic sequence from mouse chr. 1
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                          AF312994.1 GI:18182288
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2 (bases 1 to 119191)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama, A., Yada, T., Tot
Homo sapiens genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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(12-OCT-2000) Genome Analysis,
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26845 c 25557 g
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53.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45.8; DB 9;
Pred. No. 0.34;
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Institute of Molecular
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                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-DEC-1999) Department of Biochemistry, University, Beckman Center, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF216973 20796 bp
Drosophila melanogaster 1(2)01289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Manning,G., Micklem,D.R. and Krasnow,M.A.
Sequence of 1(2)01289 genomic locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manning, G., Micklem, D.R. and Krasnow, M.A.
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AF216973
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                                                                                                                                                  Join(<865..1470,3154..3310,3382..3548,3980..4015,6598..6780,6911..7054,7117..7250,7315..7495,7567..7881,8252..8566.8627..9271,9325..9507,9575..9712,9776..9958,15122..15253,15483..15806,15871..16059,16118..16255,17488..17670,17723..17854,18603..18759,16318..18983,19047..19203,19257..19423,19484..19666,19733..20489)
/product="1(2)01289 H9 form"
join(1257. .1470,3154. .3310,3382. .3548,3980. .4015,
                                                                                      /product="1(2)01289 long form"
join(<1153. .1470,3154. .3310,3382. .3548,8252. .8566,
8627. .9271,9325. .9507,9575. .9712,9776. .9958,10019.
                                                                                                                                                                                                                                                                                                       /gene="1(2)01289"
                                                12437. .12919,13190. .14706)
/gene="1(2)01289"
                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49622 c 49154 g 65819
                                                                                                                                                                                                                                                                                                                                                                                               .20796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45.8; DB 10; Length 228283; Pred. No. 0.35; 0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, complete cds,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alternatively
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Query Match
Best Local Similarity
141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                                                                    6413
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKILOKIIEDTDFVAVLFCEDHETCPPRVMDKQOCRKCAKALOELENIDDEADOLGI
GFVKIEDEALADEYNLGNIPALVYYRHOTPIIYEGELOREEDVLEWLVQKKSTGDEDD
VIEDVTSKTISCTLISKULDLIVVLFYDHGNDDSMTVLEBLEQIDDDCDKHGIQFVKIED
AKAAADYGIDSIPAIVYFEKEIPNVYDGDLMDEEQILKWLLGQLERDEIEDVTDEMLD
TMIKEGRUIAVLFYDNUNKKSQKVLEBLENIDDECDALGITFVKIDNEEAVEYGIKK
VPKLIYFEKGIPTIVENLEDBEKLLKWLTDGTSSDQLEDITDEMLDLIIEKMHYVAV
LFYDNDQKKSQKILAELENIDDECDQNDIAFVKIDDEKAKEMGIDEIPSIVLFERGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHIYEGDLMKEDELLGWLVHQKRYSEIPEVTDEMKDKLVENTEHLAVIFYDKDDKQDM
RILNELENIDDELEKEGIVIVRIDNAAEAKEYGLDHLPALIYFENKIPALYEGDLMNE
DEVLEWLLVQKKTATIEEVTDEILVTLINEHEYVVVFFTGPCEPGETCEHTLNALESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6598. .6780,6911. .7054,7117. .7250,7315. .7495,7567. .7881, 8252. .8566,8627. .9271,9325. .9507,9575. .9712,9776. .9938, 15122. .15253,15488. .17670,17723. .17854,18603. .18759,18817. .18983, 19047. .19203,19257. .19423,19484. .19666,19733. .19920)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEHLAVIFYDKDDKODMRILNELENIDDELEKBGIVIVRIDNAAEAKEYGLDHLPALI
YENNKLPALYEGDLMNEDEVLEWLLVQKKTATIEEVTDEILVTLINEHEYVVVFFTGP
CEPGETCEHTLNALESSIDDELDEAGIIFVTTEDDTGIAKKYNVKTYPRLVFFTNADELF
FTGDLDDEDEVLAWITDDETLEIPGKIEEVNVKMLDKILAENDHVVVFFYAEGDKKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMFGIDFVKIASIQAAKKYEIVNIPSLVYFRKQVPVLYDGDLHQHDKVITWLTSQDVF
EIKNEIEEVNRKMLDKLLEENEFLAVFFYEHNQPDSTAALEKLENIDSETDNLDITFV
KMADSRYAKKWGVTKLPAMVYFRRRFPSIYRGDLLSEDEVLEWLRKNRFRQPELNIFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GELSEEEEVLQWLITQKTEDRIELITRQMLETMVEETQYLAVYFYKINCNICDQILEG
LELIDDECDVFGIHMVKIQDPQLAKRYSIKTFPALVYFRNGNPLLFEGDLQNEQSVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGLTYFRKGKY INYDGDIDDEEEVLDWLTSPANMEMTDHIEQVNRKMFEKIRKNSDYV
AVIFYSDECKQCPKULÆVEHLDDEADKAGIDFVKIDDKQMAKEGVFALPAIVFFKP
TSKEEPVIYAGDLYEEEGILTWALIQKQDPSGDYIEDLEGERLVHLIEESGSIAVVEYS
GCEQCTKVLEELENIDDDCDKHGITFVKTRDFSVADGYGVHEYPALVYFEGGIPNVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IESVDRKTLQVLINDVEHLAVFFYDDECESCSDILEELENIDDDTDKHGIQFVKSNDV
KLAHEIGIFAFPALVYYETGVPINYDGNIASNQDVFNWILEQKADQSIQLINRDQLFE
YIGTKDFLAVVFYKEDDPDSPRVLRHIELIDDEAAEYGIYIVKMHDKLMAKKYGFRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDELDEAGIIFVTTEDTGIAKKYNVKTYPRLVFFRNRDPLHFTGDLDDEDEVLAWITD
DETLEIPGKIEEVNVKMLDKILAENDHVVVFFYAEGDKKAQKILNELENIDDECEEKD
IDFVKTSDDDIDKEYDLPGLPALAFYRHKFRTIYTGDLMKEEEILEWVIDLHESTADV
                                                                                                                                                                                                                                                                                                                                                                                                                                    QKNDECFYVGLGHDGHSAKRGNNFVPNDYKPFQCCPTKLEKSTKVPKMTAQRIGHSEG
DQGKRPSGGNFQFASQASSKSSTKPAAIKKQAKPSKDTDDDDEDDEDKPLVKVSYANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEILEWVIDLHESTADVIESVDRKTLQVLINDVEHLAVFFYDDECESCSDILEELENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDKRLAKQYGIKNFPALTYFREKEPIIYDGDLMDEEGVLDFLTSLEAMDLPDRIEEV
NAKILQKIIEDTDFVAVLFYDKDQKKSQKILAELENIDDECDQNDIAFVKIDDDKEAK
EWGIDEIPSIYLFERGIPHIYEGDLMKEDELLGWLVHQKRYSEIPEVTDEMKDKLVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mtftrlktlsllvcallalsfpgHVSGaGNNNNKKGSQPVAPPE
PEAVIEEVNAKQLEKLLADKDYVAVFWYARSCVTCDKVLAELEKIDDDTDSFGVDFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="1(2)01289 H9 form"
/protein_id="AAF34747.1"
/db_xref="GI:6984066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YALIALAVAFVYYTAFILQCEKPAPPPPVQHPKQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLIDDDNRELADEIEEVNERMLDRLMAESTLLVVFFYDDDCAECEEILEELEEIDGEA
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INDKRLAKQYGIKNFPALTYFREKEPIIYDGDLMDEEGVLDFLTSLEAMDLPDRIEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="1(2)01289 long
/protein_id="AAF34746.1"
/db_xref="GI:6984065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDDTDKHGIQFVKSNDVKLAHEIGIFAFPALVYYETGVPIMYDGNLKNENRVLQWLVN
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/gene="1(2)01289"
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                                                                                                                                                                                                                                                                                                                                                                                                   ?SGGSNKPQAGKKPVGKGQDNDDQSQEVEKVSKQKSAKKSGKLNVKSGYLSVGVRQQF
                                                                                                                                                                                                                                                                                                                    4444 c
                                                                                                                                                 12.1%;
49.6%;
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.9271,9325. .9507,9575. .9712,9776. .9958,10019. .10069,
7. .12919,13190. .13227)
                                                                                                                                                                                                                                                                                                               4308 g
                                                                                                                                                     Score 45.2; DB 3; Pred. No. 0.45;
                                                                                                                    Mismatches 118;
                                                                                                                                                                                                                                                                                                                        5631 t
                                                                                                                                                                                           Length 20796;
                                                                                                                    Indels
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                                                                                                                Gaps
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ACCESSION

BASE COUNT ORIGIN

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REFERENCE
AUTHORS
TITLE
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ORGANISM
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AC014497
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                                                      DEFINITION
                                                                                                AC116976/c
                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70828 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACAAGGACGAGGATAACGA 70887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10850 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 10903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10670 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACAAGGACGAGGATAACGA 10729
                                                                                                                                                                                               71008
                                                                                                                                                                                                                                                                                                                                                                                       70888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                                                                                          261 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
                                                                                                                                                                                               AGAAGATAATAATGAAGACGACGAAGGACGATGAGGATGAAAAACGACGAAGATGA 71061
                                                                                                                                                                                                                                         TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
                                                                                                                                                                                                                                                                                           CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA 71007
                                                                                                                                                                                                                                                                                                                                                                                       AGAAGATAATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA 70947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.
1 (bases 1 to 87767)
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AC014497
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ACLI6976 132000 bp DNA linear HTG 05-APR-20 Dictyostelium discoideum chromosome 2 map 2066573-2198571 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces. AC116976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rockville, MD, USA
This sequence was identified as CDM:10210380 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC014497.1 GI:6436838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or further information on this sequence e-mail to fly@celera.com NOTE: This is a 'working draft' sequence. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the finished sequence as soon as it is available and the accession number will be preserved.
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/db_xref="taxon:7227"
19624 c 19272 g 23855 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.2; DB 2; Length 87767; pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the submitter.
                                                                                  HTG 05-APR-2002
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Db 124142 AAAATTCAACATCAAATAATAATAATAATAGTGGAGGTAAAAATAAAAATAAAAATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110;
                                                                                                                                                                            ACUU/624 167062 bp DNA linear HTG 13-DEC-1999 Drosophila melanogaster chromosome 2 clone BACR10F15 (D621) RPCI-98 10.F.15 map 42E-43A strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (05-APR-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
                                          Drosophila melanogaster
                                                                                           HTG; HTGS_PHASE1.
                                                                                                                                                                                                                              AC007624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 132000)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K. Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and Noegel, A.A.
                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                 Drosophila melanogaster.
                                                                                                             AC007624.5 GI:6563437
                                                                                                                                       AC007624
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  Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agency : Deutsche Forschungsgemeinschaft (DFG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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Endopterygota; Diptera; Brachycera; Muscomorpha;
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/chromosome="2"
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G. Butenhoff,C., Champe,M., Chavez,C., Chew,M., Classiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., K.I.,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, I Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, I, Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory, MS 64-121, Berkeley, CA 94720, USA On Dec 13, 1999 this sequence version replaced gi:5670596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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1 (bases 1 to 167062)
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of 3302
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of 970 bp in length
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Pheyptoridea; Drosophilidae; Drosophila.

E 1 (bases 1 to 181771)

S Celniker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Nunoo, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
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24223 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 24170
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                                                                                                    321 TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
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Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Submitted (02-AUG-1999) Drosophila Genome Center (02-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler, Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaverl,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 2R, region 42D-42E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory, MS 64-121, Berkeley, CA 94720, USA On Sep 6, 2001 this sequence version replaced gi:13374651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley, CA 94720
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Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                     Score
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45.8
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// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:
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// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:
// SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                    ABL06114
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AAT89345
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AAZ23891
AAZ23896
                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                 Description
                    DNA encoding novel
Human p160 cDNA 16
Human p160 cDNA 16
                                                                                                                               Murine LOBO genomi
                                                                                                                                                                      Platelet binding i
                                                                                    Human ovarian anti
                                                                                                        Drosophila melanog
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bone marrow	AAK4355	22	315	9.9	7.	45
æ	AAK1773	22	315	•	7.	44
9 for	ABA3640	22	315	•	7.	43
foetal li	ABA6	22	315	9.9	7 .	42
reast	ABA5	22	315	•	7.	41
	AAH6:	22	305107	•	7	40
Shrimp white spot	AAH6:	22	3543	•	7.	39
Plasmodium falcipa	AAA7	21	2658	٠	7.	38
DNA encoding novel	AAS64269	23	1622	10.0	7	37
Listeria monocytog	ABA	24	2944528	•	7.	36
ω.	AAS9	23	1072		38.4	35
Arabidopsis thalia	AAC476	21	1448		38.6	34
encoding	AAS685	23	963		39	S S
encoding	AAS754	23	400		39	32
encoding	AAS754	23	234		39.2	3 1
encoding	AAS7546	23	654	•	39.4	30
encoding		23	654	•	9.	29
encoding nove	_	23	654	•	9.	28
encoding nove	AAS90	23	354	•	9	27
lone		19	137507		9	26
R DNA (nuc		20	32207		9	25
co.		24	3489	•	9.	24
otide sequen		22	3489	•	9.	23
i's sa	AAA3029	21	3489		9.	22
#2782 used	AAI0279	22	1944	•	9.	21
#2917 used	AAI3423	22	1944		9.	20
#2807 for q		22	1944	٠	9	19
#2825 for q	ABA2435	22	1944		७.	18
foetal	ABA5457	22	1944		9	17
breast	ABA4412	22	94	•	9	16
#7803 used	AAI0781	22	σ	•	9	15
#16095 used	AAI4	22	9	10.6	39.6	14
**	AAI2211	22	766	•	9	13
#12754 for	ABA3428	22	766		9	12
foetal li	ABA6719	22	766		39.6	11
Human breast cell	ABA49279	22	766	0	9	10

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0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

18-MAR-1999; 12-MAY-1999; Saratin; medicinal leech; thromboembolic disease; intraocular lens; collagen-dependent platelet adhesion inhibition; (MERE) MERCK PATENT GMBH 28-SEP-2000. Hirudo medicinalis. posterior Platelet binding inhibitor protein Saratin encoding cDNA sequence 29-JAN-2001 AAA28180; AAA28180 standard; cDNA; 10-MAR-2000; WO200056885-A1 capsule opacification; ss. (first entry) 2000WO-EP02117 99EP-0105530 99EP-0109503 /*tag= a /product= "Saratin" /note= "Platelet adhesion inhibitor protein" /*tag= 64..375 Location/Qualifiers 375 ВP

2365589

ABA9052:

Genomic sequence

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cc encoding Saratin, an expression vector comprising the DNA sequence, a cc host cell transformed with the expression vector, antibodies immunospecific for Saratin, and methods for identifying Saratin agonists cc immunospecific for Saratin is useful for treating thromboembolic processes, cand for manufacturing a medicament for treating thromboembolic diseases. Ct is useful for preventing thrombotic diseases. Saratin is also useful for coating artificial surfaces, since use of Saratin renders them cc mon-adhesive for cells and prevents the activation of cells. It may also useful for modifying intraocular lenses in order to lessen the cc useful for modifying intraocular lenses in order to lessen the cc thrombogenecity of the lens material, for contacting the lens material for covalent crosslinking to modify the lens material. The lens material cc useful for refractive anterior or posterior chamber ocular implants, cc which may be implanted into the eye. This new type of coating avoids problems contributed by stimulated cell growth. In combination with other completely overcome posterior capsule opacification. The canting samples derived from host cell cultures or from a creating subject that generate course capsule opacification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-611629/58.
P-PSDB; AAY94746.
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361
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                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                          TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAGTATTTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCT 60
                              GTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                       GGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAAATTATTTG
                                                                                                                                                                                                                                                                                                                                                                                        TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAGTATTTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCT
                                                                                                                          ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA
                                                                                                                                                                                       ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA
                                                                                                                                                                                                                                                       GGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guessow
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Pred. No. 3.3e-99;
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RESULT 3 AAZ23896

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RESULT 2
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Best Local
                                                                                                                                                                                                                                                                                                                        diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOBO; long bones; bone development; bone extension; skull; or diagnostic; pharmaceutical; gene therapy; transgenic animal; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                 7333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ23891 standard; DNA; 49999 BP.
                                                                                                7393
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine
                                                                                                                                                                                                                                               Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 69-97; 391pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROSE/) ROSENTHAL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000
                                                                                                                        203
                                                                        263
                                                                                                                                                                       143 ATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                                                                                                                                         the method of the invention.
            CAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG
                                                                                                ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                 ATTTTGAAGAAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG
                                                                                                                                                                                                  116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOBO
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               treating and studying
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98DE-1013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP02055
                                                                                                                                                                                                           12.2%;
49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                  0;
                                                                                                                                                                                                            Score 45.8; DB Pred. No. 0.011;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aigner T,
                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wirth
                                                                                                                                                                                                  117; Indels
                                                                                                                                                                                                                        Length 49999;
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RESULT 4
ABL06114/c
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Best Local :
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                       This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described in the method of the invention.
     ABL06114;
                                                                                                                                                                       9378
                        ABL06114 standard; cDNA; 15935 BP
                                                                             Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 161-189; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1999
                                                                                                                                                                                                                                  143 ATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine LOBO homologue genomic DNA fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ23896 standard; DNA; 49999
                                                                                                                                                                  CAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                        ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG
                                                                                                                                            AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG
                                                                                                                                                                                        ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DE-1013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-EP02055
                                                                                                                                                                                                                                                                     12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hess J,
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                   Score 45.8; DB Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aigner T,
                                                                                                                                                                                                                                                          Mismatches 117;
                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wirth
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                             Length 49999;
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                              The methods
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                    9437
                                                                                                                                                                                                              9377
                                                                                                                                              322
                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                        0;
                                          RESULT 5
ABQ54916
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Matches
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                                                                                                                                                                                                                                                                                           10130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10250 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACAAGGACGAGGATAACGA
                                                                                                                                                                                      10070
                                                                                                                                                                                                                                                                                                                                                                                                10190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABB16175) and the encoded proteins
ABQ54916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                              ABQ54916 standard; cDNA; 2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15935 BP; 4219 A; 3351 C; 3394 G; 4971 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 12824; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABB62011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
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                                                                                                                                                                                                                                       321
                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                              AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAGATGA 10017
                                                                                                                                                                                                                            TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
                                                                                                                                                                                                                                                                                     CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA
                                                                                                                                                                                                                                                                                                                                    AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                                                                                                                                        AGAAGATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45.2;
                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           260
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Best Local Similarity

52.1%;

Pred. No. 0.009;

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CC polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC treating, prognosing or preventing various ovary and/or breast-related CC disorders. Such conditions include ovarian cancer and breast rencer, and CC disorders (e.g., infertility, disorders or lyin, reproductive system CC disorders, infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and CC vaginitis), immune disorders (e.g., congenital and acquired CC vaginitis), immune disorders (e.g., congenital and acquired CC immunodeficiencies, autoimmune cophoritis, systemic lupus erythematosus), CC blood-related disorders (e.g., anaemia), cardiovascular disorders, CC and urinary system disorders. Ovarian antigen polypeptides and CC polypucleotides may also be used in screening for compounds which CC modulate ovarian antigen expression or activity. The polypucleotides may GC dientification of individuals and in forensic analysis, and the CC polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenocyping. The present construction of the construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
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antibody preparation; cytostatic; immunomodulatory; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HNBVO53 cDNA, SEQ ID NO:796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 796; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000; 2000US-209467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-147878/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP41839
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Query Match

Sequence 2438

BP;

561 A; 761 C; 686 G; 427 T; 3 other; Score 44.4;

DВ 24;

Length 2438;

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RESULT 6
AAS75452
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               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1651
                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #11256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS75452 standard; cDNA; 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1771 GGAAGAAGAA 1780
                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 11256; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 CTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAAGATTAA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGGAAGAGGAAGACTTTGAGGAAGAGGAAGAGGATGAAGAGGAATATTTTGAAGA 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
forensics, gene mapping, for genetic disorders or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0540217
2000US-0649167
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     other
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       biodiversity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W.
          Claim 82; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 372 BP; 194 A; 27 C; 134 G; 17 T; 0 other;
                                           cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation,
                                                                                                                                                                                         11-DEC-1996;
                                                                                                                                                                                                                                    WO9722255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Human p160 cDNA 160.2
                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT89346;
                                                                                 WPI; 1997-341351/31.
P-PSDB; AAW31186.
                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                 19-DEC-1995;
                                                                                                                                                                                                                26-JUN-1997
                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                        p56-lck; ss.
                                                                                                                                                                                                                                                                                                                                                                   modulation;
                                                                                                                                                                                                                                                                                                                                                                               p160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT89346 standard; cDNA; 3211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GAATGCAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATCCCATAAACGGGAGTTCGAGACTCACCTAGGCAACATAGCGAAACCCCATCTGAAA 90
                                                                                                                                                                                                                                                                                                                                                               p62; cytoplasmic; T cell; B cell; development; activation;
ation; cellular response; cell proliferation; autoimmune disease;
                                   treatment of tumours
                                                                                                                   Shin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
            10;
                                                                                                                                                                 95US-0574959
                                                                                                                                                                                         96WO-US19944.
                                                                                                                                                                                                                                                                                              Location/Qualifiers 439..3156
                                                                                                                                                                                                                                                            /product= p160
/note= "160.2"
                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                /*tag=
         175pp; English
                                                                                                                   Strominger JL,
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Pred. No. 0.043;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                   Vadlamudi RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115;
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RRESULT 8
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AAT694A
AAT64
AAT6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections by pathogenic microorganisms. p160 can be used to expand T cell populations for treating infectious diseases or cancer and p160 inhibitors could reduce B or T cell responses and may be used to treat a variety of autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA sequence encodes a novel p160 (160.2) which is capable of activating transcription of a variety of genes upon activation of p62 and is capable of binding to the p62/p561pk complex to modulate Lck function in a manner similar to p62. The genes transcribed in response to p160 activation likely include those of which are involved in T or B cell development/differentiation, T or B cell activation or production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 polypeptide is also a substrate for serine/threonine kinase activity. p160 polypeptides can modulate degradation of cellular proteins e.g. cell p160 polypeptides can modulate degradation of cellular proteins e.g. cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p160; p62; cytoplasmic; T cell; B cell; development; activation; modulation; cellular response; cell proliferation; autoimmune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p160 boosts B cell response it may be used to treat disorders where this is beneficial, e.g
                                                                                                                                                                                                                                                               11-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                              W09722255-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT89345 standard; cDNA; 3901 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3211 BP; 649 A; 990 C; 948 G; 624 T; 0 other;
                                                                                                                                 (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                    19-DEC-1995;
                                                                                                                                                                                                                                                                                                                               26-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p56-lck; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2458 GAAGAAGAGGAAGAAGAAGAAGAAGAAGAACTTTGAGGAAGAAGAAGAAGATGAAGAG 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p160 cDNA 160.1.
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                                                                                                                                                                                                95US-0574959
                                                                                                                                                                                                                                                                   96WO-US19944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 439..3846
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= p160
/note= "160.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; 52.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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WPI; 1997-341351/31 Joung I, Shin J,

Strominger JL, Vadlamudi RK;

of.

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ABA90521/
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rinis cDNA sequence encodes a novel p160 (160.1) which is capable of activating transcription of a variety of genes upon activation of p62 and is capable of binding to the p62/p561pk complex to modulate Lck function in a manner similar to p62. The genes transcribed in response to p160 activation likely include those of which are involved in T or B cell development/differentiation, T or B cell activation or production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 polypeptide is also a substrate for serine/threonie kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p160 polypeptides can modulate degradation of cellular proteins e.g. cell cycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p160 boosts B cell response it may be used to treat disorders where this is beneficial, e.g.
      WPI; 2002-043418/06
                                                                                                                                                                                                                                    11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                    FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence of Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA90521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. for treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation,
                                                         Bolotine A,
                                                                                                                  (INRG ) INRA
                                                                                                                                                                           11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                             12-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA90521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3901 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitors could reduce B or T cell responses and may be used to variety of autoimmune diseases, e.g. diabetes mellitus, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW31185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections by pathogenic microorganisms. p160 can be used to expand cell populations for treating infectious diseases or cancer and p160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Fig 8; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                 2000FR-0004630
                                                            Sorokine
                                                                                                                  INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 A; 1183 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                          IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; 52.0%;
                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2365589
                                                         Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.2; DB Pred. No. 0.18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactic bacterium; yogurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1128 G; 809 T; 0 other;
                                                         Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 10
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         997806 TCTTTCTGAAGA 997795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                997866 AATAGAATTACTGACAGAGCTATCAGTCACTTACAATCTTGGAAATCACGATATGGTTGG 997807
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                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB33000-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                                                                                                                                                                                                                        Human breast cell single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 1; 2504pp; French.
Penn
                             (MOLE-)
                                                                                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                     WO200157271-A2
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                disease; cancer;
                                                                                                                                                                                                                                                                                                            Human; microarray; single
                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                    ABA49279;
                                                                                                                                                                                                                                                                                                                                                                                                                                ABA49279 standard; DNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactis and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 CGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 TTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATGGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATTTTGCTGGTGATATTTCAAATGATTTTCACGGAATTTCCGAACCATTTTTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTCAAGAAGAAATTGATATTTTTCTGTCTCTTTTAAAGGATTTAAAGATTACAGATTT 997927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                             MOLECULAR DYNAMICS INC
Hanzel DK,
                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
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50.5%;
Chen W,
                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
   Rank DR
                                                                                                                                                                                                                                                                                                            probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                              expression; breast;
                                                                                                                                                                                                                                                                                                                                          probe #7974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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RESULT 11
ABA67193/c
ID ABA671
XX ABA671
XX ABA671
XX O1-FEB
XX Human
XX Human;
XX Human;
XX Homo s
XX WO2001
XX WO2001
XX WO2001
XX O9-AUG
XX O1-FEB
PR 04-FEB
PR 04-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon contacting contacting gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids contacting the probes with a collection of detectably labelled nucleic acids contacting the probes with a collection of detectably labelled nucleic acids contacting the probes with a collection of detectably labelled nucleic acids contacting the probes with a collection of detectably labelled nucleic acids contacting the probes are useful for contacting the label contacting the expression of regions of genomic DNA predicted to compare the protestant. They are useful for gene discovery, and for contacting predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater continuous contaction of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from without and information in the part of the contaction in the present contaction in the part of the contaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 7974; 327pp + sequence listing; English
 04-FEB-2000;
26-MAY-2000;
                                            30-JAN-2001; 2001WO-US00669
                                                                                                                                                                          Human; foetal liver;
                                                                                                                                                                                                        Human foetal liver single exon nucleic acid probe #15498
                                                                                                                                                                                                                                        01-FEB-2002
                                                                                                                                                                                                                                                                         ABA67193;
                                                                                                                                                                                                                                                                                                       ABA67193 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-496933/54.
                                                                                                            WO200157277-A2
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      irom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                    507
                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                    GA 506
                                                                                                                                                                                                                                                                                                                                                                                                                   GA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                       (first entry)
 2000US-0180312.
2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%;
                                                                                                                                                                          gene expression; single exon
                                                                                                                                                                                                                                                                                                        766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.6; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 T; 0 other;
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                                                                                                                                                                       nucleic acid
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                                                                                                                                                                        probe;
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RESULT 12
ABA34288/c
ID ABA342
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Best Local (
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                            congenital heart disease;
                                                                       Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                       Probe #12754 for gene expression analysis in human heart cell sample
                                                                                                                                                                                      ABA34288;
                                                                                                                                                                                                                    ABA34288 standard; DNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetal liver. The presen probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 15498; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing
WO200157274-A2
                                                                                                                                                       23-JAN-2002
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                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                      TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                      GATGGAGAGGATGATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%;
51.1%;
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                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.6; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
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0;

30-JAN-2001; 2001WO-US00666 04-FEB-2000; 2000US-0180312

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RESULT 13
AAI22114/c
ID AAI221
XX AAI221
XX AAI221
XX AAI221
XX Probe;
KW Probe;
KW Cervic
XX Homo s
PN WO2001
XX WO2001
XX
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Best Local S
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems, cardiovascular disease, hypertension, cardiac arrhythmias and
              09-AUG-2001
                                                                                                  Probe; human; microarray;
                                                                                                                        Probe #12047 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                      WO200157278-A2
                                                                                        cervical cancer;
                                                                                                                                                   12-OCT-2001
                                                                                                                                                                            AAI22114;
                                                                                                                                                                                                   AAI22114 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                   SG
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 190 A; 299 C; 36 G; 241 T; 0 other;
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                                                                                        SS
                                                                                                                                                                                                     DNA;
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                                                                                                   expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                   cervical
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                                                                                                  epithelial cell;
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ID AAI47409 standard; DNA; 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                              Probe; microarray; human;
                                                                                                                            17-0CT-2001
                                                                                                                                                   AAI47409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 766 BP; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00670
                                                                                                     Probe #16095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                        367
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                             GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                                                                                                           2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 12047; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to human single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                     used
                                                                                                                            (first entry)
                                                                                                     to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%;
51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 299 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                              placenta;
                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.6; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                               antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   id probes derived
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                 508
                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                             568
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0;

WO200157272-A2

Homo

sapiens

genetic disorder;

SS

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RESULT 15
AAIO7812/c
ID AAIO78
XX AAIO78
AC AAIO78
XX Probe;
XX Probe;
XW Probe;
XW Inflam
XX Homo s
XX Ho
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
04-FEB-2000; 2000US-0180312
                                                  29-JAN-2001; 2001WO-US00661.
                                                                                                09-AUG-2001.
                                                                                                                                                   WO200157270-A2
                                                                                                                                                                                                                                          Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma t
                                                                                                                                                                                                                                                                                                                      Probe #7803 used to
                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAI07812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI07812 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 766 BP; 190 A; 299 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                   Homo sapiens.
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zing gene expression in human placenta -
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2000US-0632366.
2000US-0234687.
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Search completed: May Job time: 870 secs

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Best Local
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                    measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                          of the breast, fibrocystic changes, non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
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507
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                                                                             TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
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                                                     GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGGAGGAG
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2000US-0608408.
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2000US-0234687.
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Result
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1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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        US-08-232-463-14
US-08-574-959A-8
US-09-357-014-6
US-08-574-959A-6
US-08-574-959A-6
US-08-76-728-333A-1
US-08-76-738-2
US-08-76-738-2
US-08-76-738-2
US-08-867-941-2
US-08-867-941-1
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US-08-468-55A-1
US-09-150-741-1
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US-08-232-463-14/c
Query Match
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TOPOLOGY: linea
IMMEDIATE SOURCE:
CLONE: pTZgpt-F
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ZIP: 22313-0299
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8.9	8.9	8.9	8.9	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.1	9.1	9.1
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Sequence 27, Appl	Sequence 293, App	Sequence 295, App	Sequence 657, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 121, App	Sequence 3, Appli	Sequence 4, Appli					

Title:

ALIGNMENTS

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Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          FILING DATE:

CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                        TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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Query Match
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Matches 14; Conservative 1
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                                                                                                                                                                                  TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1156 RRRRRRR 1150
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                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 ACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTG 364
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                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 AAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAAT 124
                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                            NAME/KEY:
                                                                                                          TOPOLOGY:
                                               LOCATION:
                                                                                                                                                     LENGTH:
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                                                                                           CDNA
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AND USES THEREFOR
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70; Mismatches 123;
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Score 40.2;
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Length 3211;
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                                                                                                            Matches
                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 8:
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                                    319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
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259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                       199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/574,959
FILING DATE: «Unknown)
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/357,014
FILING DATE: 19-Unl-1999
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ
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TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDE:
AND USES THEREFOR
                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3211 base pairs
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                                                                                                            Conservative
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 Mismatches

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Pred. No. 0.0066;
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                                                                                                                                             DB 4;
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                                                                                                            83; Indels
                                                                                                                                               Length 3211;
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          Sequence 6, Application US/09357014 Patent No. 6291645
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                             FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGOUTAS, ANY E.
NEGISTRATION NUMBER: 36,207
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: 652 POLYPEPFIDES, RELATED POLYPEPTIDE:
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                         199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                     259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
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     TITLE OF INVENTION:
                                                                                           APPLICANT:
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                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                   319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                          259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
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APPLICATION NUMBER: US/09/357,014
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MEDIUM TYPE: Floppy disk
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LENGTH: 3901 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD
                                                                                         Bohenzky, Roy A.
                                                                                                           Chang, Yuan
                                        Moore, Patrick S.
                                                      Edelman, Isidore S.
                                                                          Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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(617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3847
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Pred. No. 0.0073;
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DB 4; Length 3901;

83;

Indels

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Gaps

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RESULT 7
US-09-298-568-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
                                                                                                            GENERAL INFORMATION:
                                                                                                                              Sequence 1, Application US/09298568 Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
      APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                               1051 GAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAGGATGACGAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                            991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.6%;
Local Similarity 47.2%;
REFERENCE:
                                                                                                                                                                                                                                                                           GAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATGACAATAAGGAT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGAAGCATCCAAGAATGAAAAAGAATGTTCCGAAAATAATCAGGCTGGCGAGGATAAT 930
                                                                                                                                                                                                                                                                                                                                                                   TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGGAGGAGCAGGAGACAGATGAGGAGGACGAGGAGGAGGAGGAGGACGAG 1050
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16412-10001R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3489;
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SEQ ID NO 1
LENGTH: 3489
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Best Local Similarity
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CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDE
TITLE OF INVENTION: HERPESVIRUS
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 GAAGTTGATGAAGA 371
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                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                             10036
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5849564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                          US/08/770,379
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

STRANDEDNESS:

double

nucleic acid

32207 base pairs

TOPOLOGY: TYPE: LENGTH:

linear

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RESULT 9
US-08-757-669A-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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                                TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21066 GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATGACAATAAGGAT 21007
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                    SEQUENCE CHARACTERISTICS:
                                                                                    REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                     NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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1185 Avenue of the Americas
32207 base pairs
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Russo, James J.
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                                                                   (212) 278-0400
                                                                                                                                                                                                                                                                                               Floppy disk
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 20
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Best Local Similarity 47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-0
                                                                                                                                                                                                             21126 GAAGAAGCATCCAAGAATGAAAAAGAATGTTCCGAAAATAATCAGGCTGGCGAGGATAAT 21067
                                         21006 GATGAGGAGGAGGAGGAGAACAGATGAGGAGGAGGAGGATGACGAGGAGGATGACGAG 20947
                                                                                                                          21066 GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATAAGGAT 21007
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                 238 GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                    178 GAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTT 237
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                                                                                                                                                                                                                                                                                                                    Local
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                 120;
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20; Conservative
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                                                                                                                                                                                                                                                                                               Score 39.6; DB Pred. No. 0.03; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.6; DE Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                      DB 4;
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US-08-766-738-2
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Best Local 9
                                                                                                                                                                                                                                                                 Matches
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APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K
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                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: Consei
CLONE: 1813361
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LENGTH: 966 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
   373
                                                                                                                                                                                                                            193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                       703 GACGACGATGAAGTCAGTGAGGAAGGAAGAATTTGGACTTGATGAAGAAGATGAAGAT 762
                                                                                                               643 GGTGAAGAAGAGGAGTTTGATGAAGAAGATGAAGATGAAGATGTAGAAGGGGATGAG 702
                                                                                                                                                                                         583 GTTGATNAAGANGAGGAGGACGGAGAAGGAGAAGATGAGGAAGACGAGGACGATGAGGAT 642
                                                                                                                                                  253 GACCAAGAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
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OPERATING SYSTEM:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                 Match 9.6%;
Local Similarity 49.5%;
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   TA 374
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                                                                      GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                              Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
linear
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NI: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
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Pred. No. 0.077;
0; Mismatches 92; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                 643
763 GA 764
                                373 TA 374
                                                                703 GACGACGATGAAGTCAGTGAGGAAGAAGAAGAATTTGGACTTGATGAAGAAGATGAAGAT 762
                                                                                                                                                               253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                                                                                                                                               193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                    CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                 LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                               GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                GGTGAAGAAGAGGAGTTTGATGAAGAAGATGAAGATGAAGATGTAGAAGGGGGATGAG 702
                                                                                                                                                                                                GTTGATNAAGANGAGGAGGACGGAGAAGGAGGAGAAGATGAGGAAGACGAGGACGATGAGGAT 642
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Pred. No. 0.077;
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                                                                                                                                                                                                                                                                                                  DB 4; Length 966;
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US-08-867-941-2

RESULT 13

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                                                                                                                                                             RESULT 14
US-09-074-658-2
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Best Local Similarity 52.2%;
Matches 105; Conservative
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                                                 GENERAL INFORMATION:
APPLICANT: LOOSMORO
APPLICANT: Run-Pan
APPLICANT: Quijun I
                                                                                                                       Sequence 2, Application US/09074658 Patent No. 6184371
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APPLICANT: LOOSMO
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                         2077 TATCTGTTAACCGAAGACTTCACCCCAGAA-----GATGATGACGATGATTTGACCGCA 2130
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                 APPLICANT:
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TITLE OF INVENTION:
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OPERATING SYSTEM:
SOFTWARE: Patenti
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EDNESS: single
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Yang, Yan-Ping
Klein, Michel H
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               Quijun Wang
Yang, Yan-Ping
Klein, Michel H
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                                                                      Run-Pan Du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                       Loosmore,
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LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                         Sheena M
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Pred. No. 0.25;
0; Mismatches
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US-08-867-941-1
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                                                                                                                                                                                                                                                                             Sequence 1, Application US/08867941 Patent No. 5977337
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2017 AAAAAGGACAAAGGTTATAGCAATAATGAAGAAAACCATCAAGAAAAAAAGGCCATCAAGAT 2076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                                                      TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 67
                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAAT 231
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SOFTWARE: Patenti
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CITY: Toronto
STATE: Ontario
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                                                      STATE:
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                                                                       CITY: Toronto
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                                                                                                       ADDRESSEE:
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Similarity 52.2%;
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Yang, Yan-Ping
Klein, Michel H
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                         Sim & McBurney
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Search completed: May 5, 2003, 17:46:42 Job time: 76 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-115
FELECOMMUNICATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7650 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear US-08-867-941-1
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 35; DB 2; Length 7650; Best Local Similarity 52.2%; Pred. No. 0.42; Matches 105; Conservative 0; Mismatches 90; Indels
                                                                            2217 TATCTGTTAACCGAAGACTTCACCCCAGAA-----GATGATGACGATGATTTGACCGCA 2270
                                                                                                                                                                                                                                                                                                                        2271 TCTGATGATTCACAAGATGATGATGCACATGGCGATGATGATTTGATTGCATCTGATGAT 2330
                                                                                                                                                                                            292 AATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAG 351
                                                                                                                                                                                                                                                                    232 GTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAA 291
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Result.
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 700, App
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Sequence 2, Appl.
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Sequence 4255, Ap
Sequence 1125, Ap
Sequence 15076, A
Sequence 332, App
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Sequence 28059, A
Sequence 19, Appl
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Sequence 19608, A
Sequence 2825, Ap
Sequence 21723, A
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w	AGGGTAAAG AGGAGGAGG	ACCAAGAAA AGGAGGAAG	CTACATCGTTTTTGAAGAC CAACAGCAGTGATGAAGAG	similarity 6; Conser	34.8 9.3 5361 9 US- 34.6 9.2 448 10 US 34.6 9.2 8391 9 US- 34.6 9.2 8391 9 US- 34.6 9.2 8391 9 US- 34.6 9.2 1691139 9 US- 34.4 9.2 845 9 US- 34.4 9.2 1845 9 US- 34.4 9.2 1845 9 US- 34.4 9.2 1845 10 US 34.2 9.1 659158 9 US- 33.8 9.0 1824 10 US 33.6 9.0 305 10 US 33.4 8.9 451 10 U
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     Query Match
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT FILING DATE: 2001-05-23
                                                                                               OTHER INFORMATION: MAP TO ALO08720.1
OTHER INFORMATION: EXPRESSED IN BYATA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BYLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.0
OTHER INFORMATION: SWISSPROT HIT: P17164, EVALUE 4.10e+0
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00667
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R OF SEQ ID NOS: 49117
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APPLICATION NUMBER: US 09/632,366
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NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: PCT/US01/00668
TITING DATE: 2001-01-30
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                          Sequence Listing Engine vers. 1.1
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 09/632,366
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
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                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                   2001-01-30
                                                                                                                                                             2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%;
51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 1944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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TYPE: ....
ORGANISM: Homo Sapie...

FEATURE:

OTHER INFORMATION: MAP TO AL033533.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DS060/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5790, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
                           PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                           PRIOR APPLICATION NUMBER: 08/420,856 PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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SOFTWARE: Annomax Sequence Listing Engine vers.
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 GAAGAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 GATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 ATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 TTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 9.9%;
Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                             Rosen, Craig A. Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37.2; DB Pred. No. 0.43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 315;
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CCATION: (337)

CCATION: (337)

NAME/KEY: misc feature

LCCATION: (345)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LCCATION: (346)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LCCATION: (346)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LCCATION: (348)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LCCATION: (368)

OTHER INFORMATION: n equals a,t,g, or

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature
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                                                                 NAME/KEY: misc feature
LOCATION: (396)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (127)
OTHER INFORMATION: n equals a,t,g,
   NAME/KEY:
LOCATION:
                                                                                                                                    LOCATION: (395)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (330)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                        LOCATION: (394)
OTHER INFORMATION: n equals
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LOCATION: (375)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                  OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                        NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (388)
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LOCATION: (387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: (337)
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LOCATION: (211)
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misc feature (408)
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                                                                                     a,t,g,
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Best Local :
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LOCATION: (439)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (487)
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,9,
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (423)
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                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g, or
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130 CATTTCATGTAATTACCTTTTAATTTGAACATTTAGAACATGCTGTTAGATG 181
                                     151 GAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                                                                                          9.8%;
Local Similarity 50.6%;
hes 87; Conservativo
                                                                                                                   91
                                                                                                                                                           10 CTAGGATTCTAAGTAATCTAAACCCCTGCCCCAGGTAGCCAAGAATCAAGTTTGTTGTAC 69
                                                                                                                                                                                                 31 CTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTT 90
                                                                                                               TACGCGAACAGAAAATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGAC 150
                                                                             TCCCAGCACAAAAGAGATTGTCTTAGATAAGACAGTAAAGAGAATTGTATATCATNAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a,t,g,
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                                                                                                                                                                                                                                       Score 36.6; DB 10;
Pred. No. 0.82;
0; Mismatches 85;
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                                                                                                                                                                                                                                                                               Length 499;
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US-10-015-219-700 RESULT 6

Sequence 700, Application US/10015219 Publication No. US20030008299A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1

CURRENT APPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02

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                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: n = A,T,C or G US-09-777-564-700
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; NAME/KEY: misc_feature
; LOCATION: 66, 201, 213, 225, 251,
; LOCATION: 313, 322, 339, 373
; OTHER INFORMATION: n = A,T,C or G
US-10-015-219-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-777-564-700
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                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Fa
SEQ ID NO 700
LENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 700, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 700
LENGTH: 381
TYPE: DNA
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                               Query Match
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CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(381)
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                               Local Similarity
 GACGACGATGAAGTCAGTGAGGAGGAAGAAGTTTGGACTTGATGAAGAAGATGAAGAT 200
                                GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                    GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGATGAG
                                                                                                     GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG
                                                                                                                                       GTGGATGAAGAGGAGGACGAAGAAGGAGGAAGATGAGGAAGACNAGGACGATGAGGAT 80
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                                                                                                                                                                                                         Score 36; DB 10; Length 381; Pred. No. 1.1; O; Mismatches 92; Indels
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703 GACGACGATGAAGTCAGTGAGGAGGAAGAAGTTTGGACTTGATGAAGAAGATGAAGAT 313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGAT 372

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583 GTTGATNAAGANGAGGAGGACGGAGAAGGAGGAGGAAGATGAGGAAGACGAGGACGATGAGGAT 642

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253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312

GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGGATGAG

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US-10-213-700-2
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                                                    Matches
                                                                                       Query Match
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0177 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                  90;
                                                                        Similarity
                                                                                                                                                                      CLONE: 1813361
                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/766,738 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/213,700 FILING DATE: 06-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                      LIBRARY: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                TELEX:
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                            <Unknown>
                                                                    9.6%;
                                                    0;
                                                                      Score 36; DB 9; Pred. No. 1.7;
                                                    Mismatches
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                                                    92; Indels
                                                                                         Length 966
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US-09-864-761-21008/c
US-09-864-761-21008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 21008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR APPLICATION NUMBER: US 60/180,312
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 204
                 R INFORMATION: EXPRESSED II
R INFORMATION: EXT_HUMAN H
R INFORMATION: EST_HUMAN H
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Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank, David R.
                 ON: EXPRESSED IN PLACENTA, SIGNAL = 1.3

ON: EXPRESSED IN HEART, SIGNAL = 1.4

ON: EXPRESSED IN HEART, SIGNAL = 1.5

ON: EXPRESSED IN BY474, SIGNAL = 1.5

ON: EXPRESSED IN BRAIN, SIGNAL = 1.9

ON: EXPRESSED IN BOME MARROW, SIGNAL = 1.3

ON: EXPRESSED IN LUNG, SIGNAL = 1.6

ON: EXPRESSED IN HELA, SIGNAL = 1.9

ON: EXPRESSED IN HELA, SIGNAL = 0.97

ON: EXPRESSED IN HELA, SIGNAL = 0.97

ON: MT HIT: AF155827.1, EVALUE 1.60e+00

ON: EST_HUMAN HIT: BE889896.1, EVALUE 2.80e+00
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RESULT 10
US-09-864-761-4255/c
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Matches
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SEQ ID NO 4255
LENGTH: 474
                                NUMBER OF SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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APPLICANT:
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                        PRIOR
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                                                                     PRIOR FILING DATE:
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R FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/USO1/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                 APPLICATION NUMBER: US 09/608,408 ETILING DATE: 2000-66-30 APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                           FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
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                                                                                                                                        FILING DATE:
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                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670
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                                                   OF SEQ ID NOS: 49117
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                                  Annomax Sequence
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Chen, Wensheng
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2000-09-21
VITMBER: US 09/608,408
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                                Listing Engine vers.
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Pred. No. 0.88
0; Mismatches
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US-09-770-445-544/c
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                                                                                              SEQ ID NO 544
LENGTH: 876
Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
                                                                                                                                          PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                    TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: thaliana FILE REFERENCE: 2023US (PARA-012PRV)
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                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                   Hoffman, Neil
Hurban, Patrick
                                                                                                                                                                                                                                                                                                    Allen, Keith
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Slader, Ted
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Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G.
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Price, Jennifer L.
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Hamilton, Carol
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N: EXPRESSED IN BT474, SIGNAL = 1.5

N: EXPRESSED IN BARIN, SIGNAL = 1.9

N: EXPRESSED IN HONE MARROW, SIGNAL = 1.3

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HBL100, SIGNAL = 1.7

N: EXPRESSED IN HBL100, SIGNAL = 0.97
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IN HEART, SIGNAL = 1.4
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Pred. No. 1.4;
 Score 35.4; D
Pred. No. 2.4;
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                DB 10;
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                 Length 876;
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RESULT 13
US-09-878-574-15076
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
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LENGTH: 1092
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: zhu, Tong
APPLICANT: zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                             941 TTGTGTATAAACTGAAAGAAATGGGTAAGATTGATGAGAAAGATATTTCTGGGATAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 CGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTG 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
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Pred. No. 2.7;
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RESULT 15
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-332
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US-10-184-644-332
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Baul
APPLICANT: Gurney, Austin
APPLICANT: Pan, James
Sequence 332, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - NUMBER OF SEQ ID NOS: 612 SEQ ID NO 332
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CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
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                                                                                                                                                                               318 AGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAG 370
                                                                                                                                                                                                                       165 PGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGP
                                                                                                                                                                                                                                                             258 AGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
                                                                                                                                                                                                                                                                                                        105 HLAQGASRLQVLQAQLTWVRVSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGM 164
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                                                                                                                                       225 QGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGMKGDAGVMGPPGAQG
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-184-634-332
Search completed: May
Job time : 142 secs
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
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                                                                                             225 QGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGMKGDAGVMGPPGAQG 277
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9.3%; Score 35; DB:
Local Similarity 24.3%; Pred. No. 2.4;
hes 42; Conservative 35; Mismatches
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Godowski, Paul
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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AZ550718 ENTEM36TF
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41	EV58	FW53T	sophi	w	T887	26	TS83T	PK48T	EST565790	156T	w	ENTOV49TR	ENTFJ22TF	ENTEK30TR	ENTBQ34TR	ENTDV54TR	ENTDD94TF	EST572233	ENTQD93TF	ENTKK47TR	ENTCQ25TR	ENTPR62TF	EST568938	PsB 206 L	EST569638	EST562965	EST501779	EST571814	EST573357	EST563816	EST568971	EST566565	EST563698	EST573853	EST569899	EST565030	EST565816	EST569409

ALIGNMENTS

											COMMENT	JOURNAL		TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	
night quarity sequence stop: out.	Class: shotgun High quality sequence start: 25	Seq primer: M13-Forward	DNA library	Clones are derived from the Entamoeba histolytica HM1:IMSS sheared	Email: bjloftus@tigr.org	Fax: 301 838 3543	Tel: 301 838 0208	9712 Medical Center Dr., Rockville, MD 20850, USA	The Institute for Genomic Research	Department of Eukaryotic Genomics	Contact: Brendan J Loftus	Unpublished (2000)	HM1:IMSS sheared DNA library	Determination of clone end sequences from Entamoeba histolytica	Loftus, B., Van Aken, S. and Fraser, C.	1 (bases 1 to 879)	Eukaryota; Entamoebidae; Entamoeba.	Entamoeba histolytica	Entamoeba histolytica.	GSS.	AZ550718.1 GI:11176019	AZ550718	genomic, DNA sequence.	F Entamoeba histolytica Sheared DNA Entamoel	AZ550718 879 bp DNA linear GSS 14-NOV-2000	

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                                                                                                                                            1 (bases 1 to 701)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Eraser,C.M. and Carucci,D.J.
Plasmodium yoeili EST project at TIGR
Unpublished (2001)
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                        Contact: Jane Carlton
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/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
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COMMENT

Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research

9712 Medical Center Drive, Tel: 301-530-9319 Fax: 301-838-0208

Rockville,

MD 20850,

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RESULT 3
BM165474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.malaria.mr4.org/mr4pages/index.html Seg primer: ADF.
                                              1 (bases 1 to 721)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                                                    BM165474 721 bp mRNA linear EST 04-
EST567997 PyBS Plasmodium yoelii yoelii cDNA clone PYCMN68
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                                                                                                                 Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Plasmodium yoelii EST project at TIGR Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guandinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
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/lab_host="E. coli XL-1 Blue"
/note="Vector: paP-GAL4, At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL
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                                                                                                                                                                                                                                                                                          1 (bases 1 to 881)
1 (bases 1 to 881)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1: MSS sheared DNA library
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For clone info, please contact the Malaria Research and Reference
                                                                                                                                Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                           Unpublished (2000)
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Eukaryota; Entamoebidae; Entamoeba.
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Seq primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica.
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Medical Center Dr., Rockville,
301 838 0208
301 838 3543
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First strand cDNA synthesis was completed using a 50-bc
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
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/lab_host="E. coli XL-1 Blue"
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/clone="pyCMN68"
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Pred. No. 0.00044;
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                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 TGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAA 103
                                                                                                                                                                                                                                                                                                                                                                                                          AAGATGAAGAAGATGAAGATGAAGA 98
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Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
                                                                                EST.

Plasmodium yoelii yoelii.

Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                          BM163498
BM163498.1 GI:17309179
                                                                                                                                                                                                                                                              EST566021 PyBS Plasmodium
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                                                                                                                                                                                                                                      mRNA sequence.
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/note="Yector: pHOS1; Site_1: Bst I; Constructed at The
/note isolated from broth cultures of E, histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                            236 bp mRNA linear EST 04-DEW yoelii yoelii cDNA clone PYCLF94 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                              GGATGAAGATGACGAAGAAGATGAAGATGACGAAGAAGATGAAGATGACGAAGAAGATGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAAGATGATGAAGAAGATGAAGATGATGATGACGAAGAAGATGAAGATGAAGA 112
                              Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 272)
1 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
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                                                                                                                                                                                                                                                                            BM166089 272 bp mRNA linear EST 04-DEC-2001 EST588612 PyBS Plasmodium yoelii yoelii cDNA clone PYCNC52 5' end,
       Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                            BM166089.1 GI:17299321
                                                                                                                                                                                                                                                     mRNA sequence.
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Contact: Jane Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: ADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: carlton@tigr.org
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.malaria.mr4.org/mr4pages/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl s-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of smethyl dCTP after special transcriptase in the presence of
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Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project at
                                                   Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
                                                                                                                          Plasmodium yoelii yoelii.
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Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 274)
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Fax: 301-838-0208
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/lab_host="E. coli XL-1 Blue"
/note="Vector: par-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                              Plasmodium yoelii yoelii.
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Fax: 301-838-0208
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Contact: Jane Carlton
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and
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Carlton,J.M., Daly,T.M., Long,C.A., Be
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Parasite Genomics Group
The Institute for Genomic Research
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Contact: Jane Carlton
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Prime
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Plasmodium yoelii EST project at TIGR
                        Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
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//note="vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothicoyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-tractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was escised from the HybriZAP vector and plasmid DNA
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-888-0208
                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

(bases 1 to 459)
Cariton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Fraser, C.M. and Carucci, D.J.
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//note="vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinum isothicoyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
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1 (bass 1 to 580)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B. Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                 mRNA sequence.
BM161175
                                                                                                                                                                                                                                                            BM161175 580 bp mRNA linear EST 04-DEC-200 EST563698 PyBS Plasmodium yoelii yoelii cDNA clone PYCKB54 5' end
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Contact: Jane Carlton
Parasite Genomics Group
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 648)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
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Similarity 55.1%;
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 651)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blo
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
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                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                    BM161293
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                                                                                                                                                                    KEYWORDS
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Best Local S
Matches 98
                                              AUTHORS
                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATGAAGATGACGAAGAAGATGAAGATGACGAAGAAGATGAAGATGACGAAGAAGATGA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 667)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B
                                                                                                                                                                       EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Jane Carlton
                                                                                                                                                                                                                                                           BM161293 667 bp mRNA linear EST 04-DEC-2001
EST563816 PyBS Plasmodium yoelii yoelii cDNA clone PYCKD09 5' end,
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                           BM161293.1 GI:17306974
                                                                                                                                                                                                                       BM161293
                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: ADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone info, please contact the Malaria Research and Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.malaria.mr4.org/mr4pages/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/lab_most="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated."
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Pred. No. 0.0012;
0; Mismatches 80
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                                         Search completed: May 5, 2003, 17:45:16
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Job time : 1581 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.3%; Score 50; DB 13; Length 667; Best Local Similarity 55.1%; Pred. No. 0.0012; Matches 98; Conservative 0; Mismatches 80; Indels
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                                                                                                                                                                    Unpublished (2001)
Contact: Jane Carlton
Contastitute Genomics Group
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="FYCKNUY"
/clone="FYCKNUY"
/clone=lib="PyBS"
/clone=lib="pyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/lab_host="E. coli XL-1 Blue"
/lab_host="E. coli XL-1 Blue"
/lab_host="P. coli XL-
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/db_xref="taxon:73239"
/clone="PYCKD09"
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                         Score
                                                                                                                                         573
80.5
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1: /SIDS2/gcgdata/gc
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                       AAY94746

AAR22950

AAW68010

ABB69867

AAB14260

AAY50109

AAB14259

AAB29108

AAR66769
                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Mouse Ice-4 protei
Murine caspase-12
Human interleukin-
Murine Ich-3. Mus
                                                                                                                                                                                                                                                    Description
                                                                                       Mouse Ice-4 protei
Murine caspase-12
                                                                                                                                                          S. frugiperda immu
                                                                                                                                                                               Platelet binding i
Leech antiplatelet
                                                                                                                                    Drosophila melanog
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	21	488	11.8		O,
AAG53205				J	
AAG34635	21	488	11.8	7	
AAG53206	21	450	11.8	.7	w
AAG34636	21	450		7.	N
AAG53207	21	366		7.	_
ABP00862	23	117		7.	0
AAM78435	22	961			Ψ
AAM39516	22	903	11.9	68	Ф
ABG07270	22	867		68	7
AAY41665	20	561	•	68	o
AAB94657	22	403	•	68	GI
ABB08153	23	146	•	68	4
ABB58651	22	1869		8	ω
AAB18176	21	635		8	2
ABG61879	23	610		æ	_
AAM41085	. 22	738	•	69	0
AAM41084	22	738		69	9
AAB94096	22	734	٠	69	æ
AAM39299	22	734		69	7
ABB11943	22	734		69	o
AAM39298	22	717		69	G
AAB41819	21	717	٠	69	4
ABB67502	22	3257		9	ω
ABP54656	23	674		9.	N
AAW61238	19	674		9.	щ
AAU35929	22	1167		70	0
ABB09781	23	669		70	ø
ABB09771	23	669	•		æ
ABB71954	22	367		0	7
AAU69411	23	156		0.	0
AAB95086	22	589	•		u
AAB18263	21	320		•	4
177	21	S	2		ω
177	21	7	2	•	N
B669	22	σ		73.5	_
00000000000000000000000000000000000000	ABB66916 AAG17789 AAG17789 AAG17789 AAG17789 AAB18263 AAB95086 AAU95941 ABB09771 ABB09771 ABB09771 ABB09771 AAB167505 AAB41819 AAB41819 AAB41819 AAB41085 AA	22 ABB66 21 AAG17 21 AAG17 21 AAG18 22 AAB95 22 AAB95 22 ABB71 23 ABB09 22 ABB71 23 ABB09 22 AAB861 23 ABB69 22 AAB61 23 ABB65 24 AAB41 25 AAB41 26 AAM39 27 AAB61 28 AAB61 29 AAM41 20 AAM41 21 AAB68 22 AAB68 23 ABB68 24 AAM41 25 AAM41 26 AAM41 27 AAM41 28 AAM41 29 AAM41 20 AAM41 21 AAB68 22 AAB68 23 ABB68 24 AAB68 25 AAB68 26 AAB68 27 AAB68 28 AAB68 29 AAB68 20 AAB68 21 AAB68 22 AAB68 23 AAB68 24 AAB68 25 AAB68 26 AAB68 27 AAB68 28 AAB68 29 AAB68 20 AAB68 21 AA663 21 AA653		1154 22 5 175 21 5 256 21 4 158 22 3 367 22 3 367 22 3 367 22 3 367 22 1167 22 1167 22 1167 22 117 22 117 22 117 22 117 22 118 22 119	11.5 12.8 1154 22 1.5 12.5 256 21 1.5 12.5 320 21 1.6 12.3 158 23 1.7 12.3 158 23 1.7 12.3 367 22 1.7 12.2 669 23 1.7 12.2 167 22 1.7 12.2 167 22 1.7 12.1 674 19 1.5 12.1 674 23 1.5 12.0 734 22 1.6 9 12.0 734 22 1.6 9 12.0 738 22 1.5 12.0 635 21 1.5 12.0 635 21 1.5 12.0 635 22 1.5 12.0 1869 22 1.5 12.0 1869 22 1.5 12.0 1869 22 1.5 12.0 635 21 1.5 12.0 1869 22 1.5 12.0 268 22 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5

ALIGNMENTS

AY9 9-J 1-at lat ooll oost lat 0-M 8-S 8-S 7-PS	RESULT 1 AAY94746 ID AAY
AAY94746; 29-JAN-2001 (first entry) Platelet binding inhibitor protein Saratin amino acid sequence. Saratin; medicinal leech; thromboembolic disease; intraocular lens collagen-dependent platelet adhesion inhibition; posterior capsule opacification. Hirudo medicinalis. W0200056885-A1. 28-SEP-2000. 10-MAR-2000; 2000WO-EP02117. 118-MAR-1999; 99EP-0105530. 12-MAY-1999; 99EP-0109503. (MERE) MERCK PATENT GMBH. Strittmatter W, Guessow D, Hofmann U, Hemberger J, Fotev Z; Scheuble B; WPI: 2000-611629/58. WPFI: 2000-611629/58.	.T 1 4746 AAY94746 standard; Protein; 103 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or antagonists. Saratin is useful for treating thromboembolic processes, and for manufacturing a medicament for treating thromboembolic processes. It is useful for preventing thrombotic diseases. Saratin is also useful for coating artificial surfaces, since use of Saratin renders them non-adhesive for cells and prevents the activation of cells. It may also be used for coating natural collagen surfaces. Furthermore, Saratin is useful for modifying intraocular lenses in order to lessen the thrombogeneoutly of the lens material, for contacting the lens surface, or for covalent crosslinking to modify the lens material. The lens material is useful for refractive anterior or posterior chamber ocular implants, which may be implanted into the eye. This new type of coating avoids problems contributed by stimulated cell growth. In combination with other medicaments that are for instance conferring cell death, Saratin coating behavior and the coarse of the complete of coating avoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet adhesion. The invention includes polynucleotide sequences encoding Saratin, an expression vector comprising the DNA sequence, host cell transformed with the expression vector, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Saratin polypeptide and gene isolated from Hirudo medicinalis for blocking platelet adhesion, especially useful for treating or preventing thrombotic diseases, or for manufacturing a medicament for thromboembolic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 41; 46pp; English.
                                                                                                                                                                                      LAPP; collagen; platelet aggregation; antithrombotic; coronary artery disease; cerebrovascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             helps to completely overcome posterior capsule opacification. The antibody immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a treated subject. The present sequence represents the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saratin is a protein isolated from the saliva of the medicinal leech Hirudo medicinalis. Saratin is an inhibitor of collagen-dependent
               15-APR-1992
                                                                                                                                                                                                                              Leech antiplatelet protein.
                                                                                                                                                                                                                                                                                    AAR22950;
                                                                                                                                                                                                                                                                                                             AAR22950 standard; Protein; 147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                          EP480651-A
                                                                                 Protein
                                                                                                                       Peptide
                                                                                                                                                               Haementeria
                                                                                                                                                                                                                                                      10-SEP-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunospecific for Saratin, and methods for identifying Saratin agonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Saratin protein.
                                                                                                                                                                                                                                                                                                                                                                               EELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED
                                                                                                                                                                                                                                                                                                                                                                                                                                   EEREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                        EELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                               officinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                              /label= leader_peptide
/note= "21 hydrophobic
22...147
                                                                                                                                  Location/Qualifiers
                                                                 /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 573; DB 21; Pred. No. 2.3e-52;
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                                                                                            amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                               103
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                                                                                                                                                                                                     anticoagulant;
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Matches
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              Region
                                                                                 Domain
                                                                                                                                   Region
                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                  27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1990;
                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also
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When cloned into the yeast expression vector pKH4a2, the LAPP gene sequence forms a fusion product of MAF-alpha-I leader sequence plus mature LAPP, which when produced are proteolytically processed the Lys-Arg cleaving endopeptidase (KEX2), which cleaves on the claiminal side of Lys-Arg, and the products secreted into the cultured that the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. frugiperda immunophilin FKBP46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAPP blocks stimulation of platelet aggregation by collagen, at an antithrombotic concentration of about 100 nMolar (or 1.6 ug/ml). Platelet aggregation is stimulated by 2 ug/ml collagen and addition of LAPP inhibits this with an IC50 of 45nM, but this may be overcome by the addition of 0.25 mM arachidonic acid. LAPP could be used for treatment and prevention of thrombotic LAPP could be used for treatment and prevention of thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating thrombotic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant; tissue graft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW68010 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions especially coronary artery and cerebrovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 15; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-125288/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunophilin; moth; insect cell; nuclear; immunosuppression; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRN 120
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frugiperda
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative nuclear localisation signal"
135..138
                                                                                                                                                                                                                  /note= "putative nuclear localisation signal"
/note= "AP motif"
                                                                                                                                                                      215..218
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                                                                                                              /note=
                                                                  . 223
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                                                                                                              "EEAP motif"
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                                                                                                                                                                                                                                                                                                                                                                        "putative nuclear localisation signal"
"putative nuclear localisation signal"
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Pred. No. 1.1;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the immunophilin FKBP46 from the moth Spodoptera frugiperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive agents can be used in treating transplant and tissue graft patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                                                                                             Drosophila melanogaster
                                                                                                                                 pharmaceutical
                                                                                                                                                     Drosophila;
                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 36393.
                                                         WO200171042-A2
                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                     ABB69867 standard; Protein; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alnemri ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995;
31-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AA;
                                                                                                                                                 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandes-Alnemri T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JEFFERSON THOMAS
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96US-0741134.
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272..275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            localisation signal"
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AAB14260
ID AAB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL30511), expressed DNA sequences (ABL01840-ABL6175) and the encoded proteins
               Yuan
                                                                                                                                                                                                                                                                                                 ced-3; virally induced cell death; apoptosis; gene therapy; neural;
muscular degenerative disease; myocardial infarcation; stroke; agin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form specification, but was obtained in electronic f
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11-JUL-2000;
                                               (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                 04-JUL-2000
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                                                                                                                                                                                                                                           Mus sp
                                                                                                                                                                                                                                                                                                                                                             Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB14260 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 36393; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL13970
                                                                                                                           10-JUN-1994;
                                                                                                                                                                                                                                                                                 interleukin-1beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 --LDKLRAVATSSDSDENYNKSSSPDLALDLHASDVEADVDGDEAGDADEDGDADAD 198
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             J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELDQEKFVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                         Ice-4 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
             Miura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                       93US-0080850
                                                                                                                             94US-0258287
                                                                                                                                                                                                                                                                               converting enzyme; ICE; cysteine protease; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DENFTEN-----YLTDCEGKDAGNAAGTGDESDEVDED
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23.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418
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34;

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RESULT 6
AAY50109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine interleukin-lbeta converting enzyme (mICE) (AAB14259), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally
                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                        premalignant chronic lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                     Cleavage-site
                                                                                                                                                                              Key
                                                                                                                                                                                                                      preneoplastic ds.
                                                                                                                                                                                                                                                                     Caspase; splice variant; truncated; programmed cell death;
                                                                                                                                                                                                                                                                                            Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 17; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocardial infarction or stroke
          Yuan J,
                                                                        14-APR-1999;
                                                                                                                WO9952925-A1
                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                         AAY50109 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                   16-APR-1998;
                                                                                             21-OCT-1999
                                                                                                                                                         Protein
                                                                                                                                                                                                                                                              regulation;
                                                                                                                                                                                                                                                                                                                 21-JAN-2000
                              (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                           82
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                                                                                                                                                                                                sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                            caspase-12 splice variant, caspase-12L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                         lymphocytic
          Morishima N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AA;
                                                                                                                                                                                                                                       proteolytic cascade; malignant condition;
t condition; solid tumour; lymphoma;
phocytic leukaemia; prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                              liver focus; chemotherapy resistance; autoimmune disease
                                                   98US-0081962
                                                                        99WO-US08064
                                                                                                                                     /note= "<318:.319
                                                                                                                                                       Location/Qualifiers 94..95 95..419
                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                                             "Caspase-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75.5;
Pred. No. 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                      apoptosis;
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WPI; 2000-464343/40
N-PSDB; AAA72843.
                                                                                                                                     US6083735-A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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This sequence represents a cDNA encoding murine caspase-12L, a splice variant of caspase-12. Caspases are a family of proteins involved in the regulation of apoptosis and are synthesised as proforms which are activated via cleavage after specific Asp residues. Mammalian cells express several caspases, and it is thought that these act in a proteolytic cascade to cause programmed cell death. Nucleic acids encoding caspase-12s (AAZ3544) or truncated forms of caspase-12L (CAZ3546, AAZ3547) are used for production, recombinantly or in vivo, of caspase-12 polypeptides which induce programmed cell death. This is carticularly useful for treating (pre)mailgnant conditions (e.g., solid tumours, B cell lymphoma, chronic lymphocytic leukaemia, prostatic particularly useful for treating (pre)mailgnant conditions (e.g., solid tumours, B cell lymphoma, chronic lymphocytic leukaemia, prostatic particularly preneoplastic liver foci and resistance to chemotherapy), or autoimmune diseases. The caspase-12 proteins can also be used to raise specific antibodies (for example, to determine gene expression and to screen expression libraries) or as molecular weight markers. Fragments of caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used as probes to isolate the caspase-12 encoding nucleic acids can be used to raise encoding nucleic acids can be used to raise encoding nucleic acids can be used to raise encoding nucl
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ32645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating
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419
AA;
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Matches
82 EQLSLQFSNDEDD
                          95
                                                   26
                                                                           44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG
                         DE----SDEVD 101
                                                   VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ
                                                                                                    Similarity
26; Conserv
                                                                                                      Conservative
                                                                                                                  13.2%;
35.6%;
                                                                                                   14;
                                                                                                                  Score 75.5;
Pred. No. 13;
                                                                                                      Mismatches
                                                                                                      . 14;
                                                                                                    Indels
                                                                                                       19;
                                                                                                      Gaps
                                                      81
                                                                              94
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DB 20;

Length 419;

6,

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AAB14259 standard; Protein; 419 AA
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Mouse Ice-4 protein 09-FEB-2001 AAB14259; (first entry) sequence #1.

ced-3; virally induced cell death; apoptosis; gene therapy; neu muscular degenerative disease; myocardial infarcation; stroke; converting enzyme; ICE; cysteine protease; neural; mouse aging;

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Mus sp
                           interleukin-1beta
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Yuan J,
                                                24-JUN-1993;
                                                                      10-JUN-1994;
                                                                                              04-JUL-2000
                      (GEHO)
 Miura M;
                        GEN HOSPITAL CORP
                                                9308-0080850
                                                                      94US-0258287.
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RESULT 8
AAB29108
ID AAB2
XX AAB2
XX AAB2
XX AAB2
XX MUS
KW MOUS
KW CANC
XX WO20
XX WO20
XX WO20
PN WO20
PN 12-C
XX O6-A
XX UAF
XX VAI
PH YUAF
XX YAF
PH YUAF
XX YAF
PH YUAF
XX YAF
PH YUAF
XX The
PT STrC
XX The
CC Case
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The present invention is concerned with methods for identifying compounds useful for modulating caspase-mediated apoptosis. These include the caspase-12 protein shown here. These agents can be used in the treatment
                                                                                                          Caspase-12 polypeptide useful for treating apoptotic conditions e.g. stroke, ischemia and proliferated disease e.g. cancer, lacks at least amino acids in a specific region of the native amino acid sequence -
                                                                          Claim 1; Page 65-66; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequence of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine interleukin-lbeta converting enzyme (mICE) (AAB14249), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally
                                                                                                                                                                                                                                                                                                                                     06-APR-2000; 2000WO-US09173.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200059924-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; caspase-12; calpain; apoptosis; cell death; autoimmune disease; cancer; viral infection; apoptotic condition; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine caspase-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB29108 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 16; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myocardial infarction or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQLSIQFSNDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                           Nakagawa T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                 99US-0127967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 9
AAR66769
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Best Local
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                                                                                  homolog (Ice-4), increasing Ice-4s enzymatic activity can promote the programmed cell death of cancer cells (pref those overexpressing the bcl-2 oncogene), this can be used as the basis of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic activity programmed cell death can be inhibited, this may be useful in the development of new cell lines which remain viable in culture
                                                                                                                                                                                                                                              Promoting or preventing programmed cell death in vertebrate - by inhibiting the activity of interleukin-1 beta converti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of apoptotic conditions, including stroke, neurodegeneration, ischaemia, Alzheimer's disease and muscular dystrophy, and prolliferative diseases such as cancer, autoimmune disorders such as systemic lupus erythematosus and multiple sclerosis, and viral infections, particularly those associated with herpes virus, poxvirus and adenovirus. The treatment may
                                            Sequence
                                                                                                                                                                   AAQ79969 encodes AAR66769 human interleukin-1 beta converting enzyme
                                                                                                                                                                                                    Claim 24; Fig 16; 116pp; English.
                                                                                                                                                                                                                                enzyme.
                                                                                                                                                                                                                                                                                                                                   Miura M, Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human interleukin-1 beta converitng en
oncogene bcl-2; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09500160-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interleukin-1 beta convering enzyme homolog (Ice-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR66769 standard; Protein;
                                                                         for extended
                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR66769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ
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                                                                                                                                                                                                                                                                                                       1995-051742/07
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form of gene therapy.
                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA;
                                                                      or indefinite periods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                         93US-0080850
                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US06630
13.2%; Score 75.5; 35.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                   independant of growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme homolog; Ice-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
             Length 432;
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                                                                                                                                                                                                                                            converting
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Matches

Conservative

14;

Mismatches

14;

19;

Gaps

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RESULT 10
AAR98464
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                                                                                                                   Query Match
Best Local
                                                                                                        Matches
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apoptosis; interleukin-1 beta converting enzyme; gene therapy.
                                                                                                                                                                                                                                                                Ich-3 (AAR98464) causes programmed cell death and shows significant homology to mouse interleukin-1 beta converting enzyme (ICE), mouse mIch-2 (AAR98461) and human Ich-1 (AAR98462-63). Its sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-333763/33:
N-PSDB; AAT31554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09620721-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine Ich-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR98464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR98464 standard;
                                                                                                                                                                                  activity of ICE.
                                                                                                                                                                                                cDNA library. The protein can be obtd. from host cells contg. vectors that include an Ich-3 coding sequence. It can be used to control the programmed cell death of vertebrate cells, to develop cell lines that remain viable for extended periods, and to increase the
                                                                                                                                                                                                                                                                                                                      Claim 24; Fig 14; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Preventing or promoting programmed cell death in vertebrate cells comprises inhibiting or increasing the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miura M, Yuan J;
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                             interleukin-1-beta converting enzyme, or altering expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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                                                                        44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                          95
                                                   40
96 EQLSLQFSNDEDD 108
                                                                                                                                                                                                                                                   deduced from the Ich-3 gene (AAT31554) isolated from a mouse thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE----SDEVD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQLSLQFSNDEDD 108
                          DE-----SDEVD 101
                                                   VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 95
                                                                                                        26;
                                                                                                                    Similarity
                                                                                                                                                          432 AA;
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0368704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US00177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 432 AA
                                                                                                                   13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORP
                                                                                                     14;
                                                                                                     Score 75.5; D
Pred. No. 14;
14; Mismatches
                                                                                                                                 DB 17;
                                                                                                       14;
                                                                                                                                Length
                                                                                                        Indels
                                                                                                        19;
                                                                                                                                                                                                                                                                    sequence
                                                                                                       Gaps
                                                                                                        6;
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RESULT 11 ABB66916

Protein identification; signal transduction pathway; metabolic pathway;

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RESULT 12
AAG17789
ID AAG1
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XXX DXXXX
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Matches
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG156-ABL30511), expressed DNA sequences (ABLIG159) and the encoded proteins (ABB737-ABB72072).
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 27540; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB66916 standard; Protein;
                       Arabidopsis thaliana protein fragment SEQ ID NO: 18943.
                                                                           AAG17789;
                                                                                                     AAG17789 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                  17-OCT-2000
                                                                                                                                                                     565 LVENFWRHYIQCCECQKKDACALSNPSMLGNTEYTG 600
                                                                                                                                                                                                                      505 SKKDIDFSKFFSMLDDKDKLKFRVAELMVRCMFLMEKRMQQDLKGNKVCNVEEKDNNVNQ 564
                                                                                                                                                                                                                                                12 NRKYTDFDKSFKKSSDLDECK-KTCFKTEYCYIVFEDTVNKECYYN-VVDGEELDQEKFV 69
                                                                                                                                                                                             70 VDENFTENYL -- TDCEGKDA---
                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-656860/75.
                                                                                                                                                                                                                                                                            l Similarity
27; Conserv
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                                                                                                                                                                                                                                                                                                                                1154 AA;
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                             14;
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                                                                                                        175
                                                                                                                                                                                                                                                                                          Score 73.5;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                      Length 1154;
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2000EP-0301439. 99US-0123180. 99US-0123180. 99US-0125788. 99US-0125788. 99US-0126264. 99US-0126264. 99US-0126264. 99US-0130047. 99US-0130047. 99US-0132048. 99US-0132484. 99US-0132484. 99US-0132486. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134219.	assay; genetic mapping; equence.
	gene expression control;
	promoter;
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990S-0141287. 990S-0141287. 990S-0142154. 990S-01422154. 990S-0142320. 990S-0142920. 990S-0142920. 990S-0142920. 990S-0144086. 990S-0144086. 990S-0144332. 990S-0144333. 990S-0145088. 990S-0145918. 990S-0145938. 990S-0155188. 990S-0155183. 990S-0155183. 990S-0155183.	9US-014069 9US-014082

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RESULT 13
AAG17788
ID AAG177
XX AAG17
XX AAG17
XX T17-OC
DT 17-OC
DX Arabi
XX Prote
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07-OCT-1999;
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14-OCT-1999;
18-OCT-1999;
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29-SEP-1999;
04-OCT-1999;
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22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
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10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                           Arabidopsis thaliana protein fragment SEQ ID NO: 18942.
                                                              17-OCT-2000
                                                                                 AAG17788;
                                                                                                  AAG17788 standard;
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14-OCT-1999
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                                                                                                                                                                                93
                                                                                                                                                                                         23 KKSSDLDECKTTCFKTEYCYIVFEDTVNKECYYNVVDGEEL-DQEKFVVDENFTENYLT-
                                                                                                                                             FNNDADEEDFDGDDDGDEEGEEDDDDEEEED
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                                                                                                                                                                             KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 141
                                                                                                                                                                                                                   Similarity
26; Conserv
                                                                                                                                                                                                                 12.5%;
ilarity 28.6%;
Conservative 1
                                                              (first entry)
                                                                                                                                                                                                                                                    99US-0152363
99US-0153758
99US-01547018
99US-0154779
99US-0155559
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99US-0156596
99US-0157715
99US-0157765
99US-0159339
99US-0159339
99US-0159331
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99US-0159638
99US-0159638
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99US-0159638
99US-0159638
99US-0160761
                                                                                                  Protein; 256
                                                                                                                                                                                                                 %; Score 71.5; DI
%; Pred. No. 12;
12; Mismatches
                                                                                                  AA
                                                                                                                                             172
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06-MAY-1999;
07-MAY-1999;
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04-MAY-1999;
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9908-0126264
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30-JUN-1999 01-JUL-1999 01-JUL-1999 01-JUL-1999 06-JUL-1999 06-JUL-1999 08-JUL-1999 09-JUL-1999

13-JUL-1999;

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RESULT 14
AAB18263
ID AAB18
XX AB18
AC AAB18
XX AB18
XX D7-NC
XX Plasm
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Best Local S
Matches 26
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22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
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21-OCT-1999;
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29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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16-SEP-1999;
20-SEP-1999;
           WO200025728-A2
                                                      Plasmodium falciparum; antimalaria; malaria;
                                Plasmodium falciparum
                                                                                     Plasmodium falciparum chromosome 2 related protein SEQ ID NO:120.
                                                                                                             07-NOV-2000
                                                                                                                                   AAB18263;
                                                                                                                                                         AAB18263 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT
12-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999,
22-OCT-1999,
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13-OCT
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                                                                                                                                                                                                                                                          174
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                                                                                                                                                                                                                                                                        23 KKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEEL-DQEKFVVDENFTENYLT- 80
                                                                                                                                                                                                              FNNDADEEDFDGDDDGDEEGEEDDDDEEEED
                                                                                                                                                                                                                         -----DCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                        KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 222
                                                                                                                                                                                                                                                                                                     l Similarity
26; Conserv
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                              990S-0158029

990S-0158229

990S-0159293

990S-0159295

990S-0159296

990S-0159330

990S-0159331

990S-0159637

990S-0160747

990S-0160747

990S-0160778

990S-0160778

990S-016078

990S-0160815

990S-0161405

990S-0161405

990S-0161405

990S-0161405

990S-0161351

990S-0161351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0154018
990S-0154039
990S-0155139
990S-0155139
990S-0155659
990S-0155659
990S-0156596
990S-0157775
990S-0157775
990S-0157765
                                                                                                                                                                                                                                                                                                              12.5%;
                                                    chromosome 2; human malaria parasite; vaccine;
protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                   Score 71.5; D
Pred. No. 19;
12; Mismatches
                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                         DΒ
                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                         256;
                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   4;
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99US-0141287
99US-0141287
99US-0142154
99US-0142154
99US-0142920
99US-0142920
99US-0143542
99US-0144085
99US-0144332
99US-0144332
99US-0144333
99US-0144333
99US-0144884
99US-01445086
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99US-0147303
99US-0147303
99US-0148319
99US-014936
99US-0151065
99US-0151080
99US-0151080
99US-01511330
99US-0151330
99US-0151330

26-JUL-1 27-JUL-1

23-JUL-1999

02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 13-AUG-1999 13-AUG-1999 14-AUG-1999 15-AUG-1999 17-AUG-1999 18-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG-1999

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PXXXXXEXTXXXXI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC (I) and (II) are useful for the development of vaccines against CC (I) and following the sequences of (I), are useful in the detection (I) and polyclonal antisera or a monoclonal CC consideration of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC p. falciparum. Sequencing of the Plasmodium chromosome 2 and the consideration, or they can be used to identify drug resistance in CP falciparum. Sequencing of the Plasmodium chromosome 2 and the complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite second of the control of the world, and there is a pressing need for vaccines and mosquito CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA7078 to AAA70287 and ABBH144 to ABBH352 represent nucleotide CC and protein sequences given in the present invention, but which are not cc.
                                                                                                                                                                                                                                           AAB95086
                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365347/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998;
EP1074617-A2.
                                                                                                                                                                                                                           AAB95086 standard;
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                                 Homo sapiens
                                                                       Human; primer;
                                                                                                        Human protein sequence SEQ ID NO:16999.
                                                                                                                                                  26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FYANRKY -----TDFDKS ---- FKKSSDLDECKK ---- TCFKTEYC ------
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CARUCCI D.
GARDNER M.
VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                  (first entry)
                                                                       detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%;
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                                                                                                                                                                                                                             589
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Pred. No. 25;
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2000;
02-MAY-2000;
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27-AUG-1999;
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                                                                                                                            DTVNKECYYNVVDGEELDQEKFVVD------ENFTENYLTDCEGKDAGNAAGTGDES 97
EE-DED 281
                                                                                      MTRDSDGYENSTDGEMCDKDALEEDSESVSEIGSDEESENEITSV-GRASGDDDGSEDDE 276
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                                        DEVDED 103
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, Sugiyama T, Wakamatsu
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Pred. No.
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, Otsuki
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Search completed: May Job time : 59 secs

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2003, 17:50:37

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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US-08-044-134-2
US-09-187-789-16
US-09-139-600-11
US-08-258-2878-58
US-08-368-704C-56
US-08-368-704C-55
US-08-368-704C-55
US-08-170-360-1
US-08-170-360-2
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Sequence 3, Appli
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Sequence 16, Appli
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Sequence 57, Appli
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Sequence 11, Appli
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Sequence 37, Appli
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Ition US/080445. N: Olly, Thomas M eer, Paul M. ON: Protein fo ON: Collagen of CES: 1 DDRESS: Irck & Co., Inc. Box 2000 Irsey E FORM: Floppy disk PC competible EM: PC-DOS/MS- entin Release ION DATA: MBER: US/08/04 INFORMATION: Ichards: 32,586 ET NUMBER: 32,586 ET NUMBER: 180 O9-OCT-1990 NFORMATICS: MBER: US/08/04 INFORMATICS: UMBER: 32,586 ET NUMBER: 180 O9-OCT-1990 O9-	148 148 1658 17658 1726 1726 1726 250 250 25172
	4 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
US/08044547 Thomas M. Thomas M. Protein for Inhibiting Collagen-Stimulated Platelet 12 S: (CO., Inc.) 2000 Wiyy disk compatible PC-DOS/MS-DOS PC-DOS/MS-DOS AT Release #1.0, Version #1.25 ATA TRELEASE #1.0, Version #1.25 ATA US/08/044,547	US-09-362-230-36 PCT-US94-07926-36 US-09-172-841-55 US-09-355-160D-8 US-08-609-049A-13 US-08-609-049A-30 US-09-170-996-13 US-08-81-269-5 US-09-134-596-5 US-09-134-596-5 US-09-134-596-5 US-09-134-596-5 US-09-134-293-3 US-09-211-203-3 US-09-211-30-3 US-09-340-993-3 US-09-468-442-3
Aggregation	Sequence 36, Appl Sequence 35, Appl Sequence 55, Appli Sequence 8, Appli Sequence 13, Appl Sequence 13, Appl Sequence 30, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

Query Match Best Local Similarity

14.0%; Score 80.5; DB 32.7%; Pred. No. 0.21; 10;

DB 1;

Length 126; Indels

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Matches

18;

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                                                                                                                                                                    Sequence 2, Application US/08741134
Patent No. 5861498
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                             APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Collage
                                  APPLICANT: Fernandes-Alnemri, Teresa
TITLE OF INVENTION: IMMUNOPHILIN FKB
TITLE OF INVENTION: AND
TITLE OF INVENTION: METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: protein
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
                NUMBER OF SEQUENCES:
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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F: P.O. Box 2000
Rahway
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                                                                                                               Litwack, Gerald
Alnemri, Emad S.
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Collagen-Stimulated Platelet Aggregation
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                                      METHODS OF USING THE SAME
                                                                         IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
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                 δõ
                                                                                                                                 ; ORGANISM: Mus musculus US-09-187-789-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-187-789-16
                                                                                                                                                                                                    Sequence 16, Application US/09187789

Patent No. 6340740

GENERAL IMPORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
TITLE FERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16
                                       Query Match
Best Local Similarity 35.6
Conservative
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                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                          LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: Wordberfect for Windows 6.1
CURRENT APPLICATION DATA:
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LENGTH: 412 amino acids
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NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 01-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 DE--NDESFKMN--TSAEGDDSDEEDDDEDEEDEEDDD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 ANKKAKPDKKAGKNSAPAAESDSDDDD------EDQLQK-----FLDGEDIDT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place - 46th floor CITY: Philadelphia
44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ANRKYTDFDKSFKKS-----SDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pennsylvania
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                                                                           13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 80.5; DB 30.6%; Pred. No. 0.87; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 60/007,163
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                                                           14;
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                                                                           Score 75.5;
Pred. No. 1;
                                                             Mismatches
                                                                                               DB 4;
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                                                                                               Length 172;
                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus US-09-139-600-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APR
TITLE OF INVENTION: AND METHOD OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
REFERENCE/DOCKET NUMBER: 06
                               FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                          STATE: D.C
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      APPLICATION NUMBER: US/08/258,287B FILING DATE: 10-JUN-1994
                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 24-JUN-1993
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                               US 08/080,850
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                   .0609.3920001
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US-08-368-704C-56
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Best Local
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                     INFORMATION FOR SEQ ID NO:
              MOLECULE TYPE:
                                                                                                                                                                REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION
TELEPHONE: (202,371,2600
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 10-JUN-1994
                                              STRANDEDNESS:
                                                                                                                                     TELEFAX: (202) 37:
TELEX: 248636 SSK
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
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STRANDEDNESS: unl
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                                                               amino acid
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                                                                                 418 amino acids
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                                unknown
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                                                                                                                                                                                                        0609.3920002
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Pred. No. 3;
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US-08-368-704C-55
              RESULT 9
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FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.39200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                     y Match 13.2%;
Local Similarity 35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                82 EQLSLQFSNDEDD 94
                                                                                                 95 DE----SDEVD 101
                                                                                                                                   26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                 44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                     26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                       419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         : (202) 371-2600
(202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/258,287B
10-JUN-1994
                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%; Score 75.5; 35.6%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0609.3920001
                                                                                                                                                                                                                     Score 75.5;
Pred. No. 3;
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                                                                                                                                                                                                                                      DB 3;
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                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                      Length 419;
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                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                   Gaps
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; MOLECULE TYPE: protein
US-08-368-704C-55
                                                                                                                                                                                                                         RESULT 10
US-08-170-360-1
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                                                                                                                                                                                   Sequence 1, Application US/08170360 Patent No. 5656602
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                   GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0609.3920002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                 CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New CITY: Washington STATE: D.C.
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TELEFAX: (202) 371
TELEX: 248636 SSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  82 EQLSIQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                      95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                           26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                             44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 35.6%; es 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bugaisky, Lawrence B. REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
STATE:
                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/080,850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                   ADDRESSEE:
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Washington D. C.
                                 E: Rothwell, Figg Ernst & Kurz
Suite 701-E, 555 Thirteenth St.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sterne, Kessler, Goldstei
1100 New York Avenue, Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75.5;
Pred. No. 3;
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e, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 419;
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6,

COMPUTER READABLE FORM:

COUNTRY: U.S.A.

20004

MEDIUM TYPE:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn

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RESULT 11
US-08-961-083-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :NFORMATION FOR SEQ ID NO:
                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi et. al. TITLE OF INVENTION: Str
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                              APPLICATION NUMBER: US/08/961,083
                                                                   CLASSIFICATION: 435
                                                                                  FILING DATE:
                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 VDELDRCCETHDNCY---------RDAKNLDSCKFLVDNPYTESYSYSCSNTE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 LDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                    20850
                                                                                                                                                                                                                                                    Maryland
                                                                                                                                                                                                                                                                                9410 Key West Avenue
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(202)783-6031
TD NO: 1:
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                                                                                                                                                                  HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                     452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
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                                                                                                                                                                              3.50 inch, 1.4Mb storage
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Pred. No. 2.
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RESULT 12
US-08-170-360-2
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Best Local Similarity
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APPLICANT: TSeng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                  TELEFAX: (202)783-603 INFORMATION FOR SEQ ID NO:
                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
                                                                                                                                                                                                                 PRIOR APPLICATION UDATA:
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                            STRANDEDNESS:
                                                                                                                                  TELEPHONE:
                                                                                                                                                                                     NAME: Ernst, Barbara G. REGISTRATION NUMBER: 3(
                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D. C.
                                                               LENGTH:
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ELDQEKF ----- VVDENFTENYLTDCEG ----- KDAGNAAGTGDE 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,373
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                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Rothwell, Figg Ernst & Kurz Suite 701-E, 555 Thirteenth St., N.W
                                                           124 amino acids
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protein
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Pred. No. 23;
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                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-888-497-41
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Best Local Similarity
Matches 17; Conserv
                          Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                 TELEFAX: 305-764-4996 INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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ANTI-SENSE: N
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 00 FILING DATE: 26-JUL-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 200 buccase CITY: Fort Lauderdale
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ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
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 27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                            LENGTH:
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                                     Conservative
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Sequences and Low Molecular Weight Amino Acid Sequences
Encoded Thereby, Antisense Sequences and Nucleotide
Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 67; DB 1; Length 124; 22.7%; Pred. No. 5.4; tive 14; Mismatches 22; Indels
                                                  11.7%;
22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                              us 08/097,354
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                                   14;
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                                                    Score 67; DB Pred. No. 5.4;
                                     Mismatches
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                                                                   DB 2;
                                   22;
                                                                    Length 124
                                     Indels
                                     22;
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US-09-362-230-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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MEDIUM TYPE: Floppy
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LENGTH: 124 amino acids
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APPLICATION NUMBER:
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                                                                                                                                                                                                                     27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
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                                                                           87 AGNAAGTGDESDEVD 101
                                                                                                                                                      40 DLDRC---CQTHDHCY---
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SGNVITCSDKNNDCE 92
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17; Conserv
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IBM PC compatible
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                                                                                                                                                      ---NQAKKLESCKFLIDNPYTNTYSYKC----
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                                                                                                                                                                                                                                                                                                        22;
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RESULT 15 PCT-US94-07926-41

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Search completed: May 5, 2003, 17:51:12 Job time: 23 secs
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                                                                                                                                                                                                                                                                                                 Query Match 11.7%; Score 67; DB 5; Length 124; Best Local Similarity 22.7%; Pred. No. 5.4; Matches 17; Conservative 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/097,354
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 124 amino acid
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 33301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

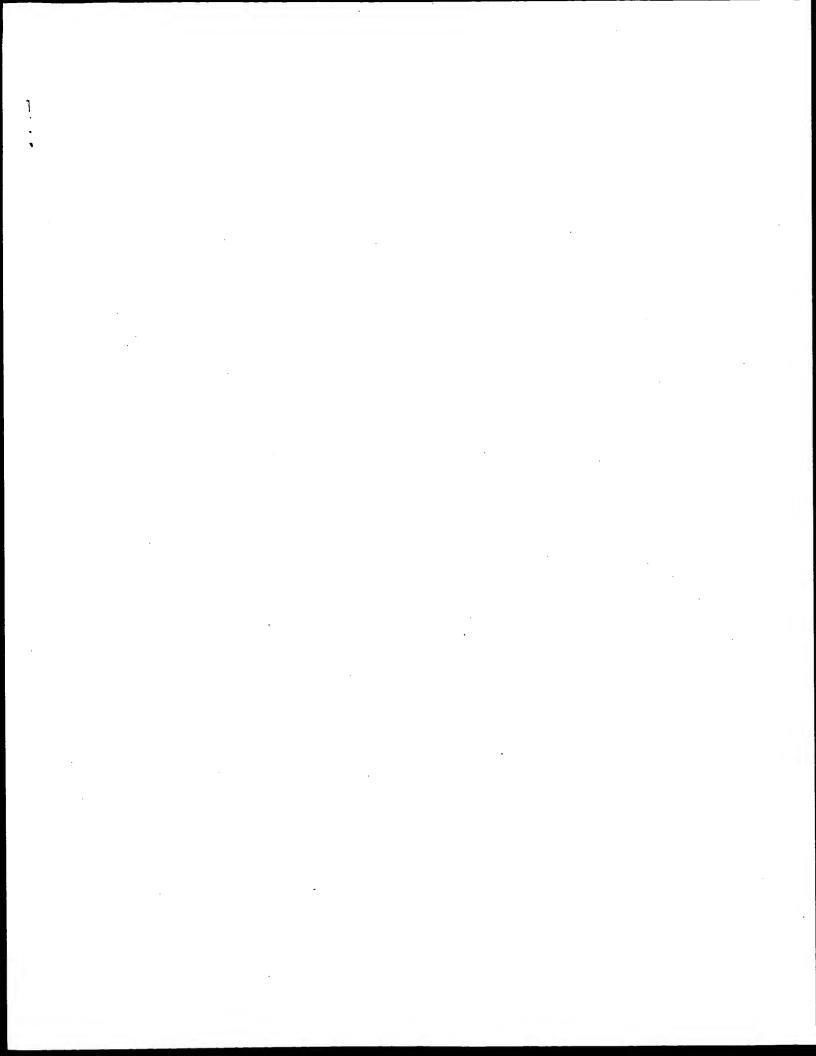
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                   78 SGNVITCSDKNNDCE 92
                                                                                                                                                     87 AGNAAGTGDESDEVD 101
                                                                                                                                                                                                       40 DLDRC---CQTHDHCY---
                                                                                                                                                                                                                                            27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard CITY: Fort Lauderdale STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 amino acids
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
              69.5
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573
1 EEREDCWTFYANRKY
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEREDCWTFYANRKYTDFDK.....GKDAGNAAGTGDESDEVDED 103
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pubpaa/pcTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US0_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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10 US-09-989-903-16

10 US-09-833-790-252

10 US-09-815-242-11522

10 US-09-815-242-122

10 US-09-765-272-200

10 US-09-993-999-7
                                         US-09-933-280-46
US-09-801-574-57
US-09-808-748-11327
US-09-974-298-114
US-09-975-458-5
US-09-975-458-5110
US-10-102-806-695
US-10-042-417-52
US-10-042-417-52
US-10-042-417-52
US-10-042-417-52
US-10-042-417-52
US-09-930-871-10
US-09-930-871-10
          US-09-930-871-18
US-09-930-871-20
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253.929 Million cell updates/sec
Sequence 16, Appl
Sequence 15, Appl
Sequence 252, App
Sequence 200, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 57, Appl
Sequence 114, Appl
Sequence 511, App
Sequence 511, App
Sequence 695, Appli
Sequence 695, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 20, Appli
Sequence 20, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20
61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	63	63	63	63	63	63
10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.0	11.0	11.0
292	273	272	272	272	270	265	251	225	143	2243	1272	1272	1172	1172	1172	1168	578	571	322	2009	1998	1973	1962	1453	1442
9	9	9	9	9	10	9	9	9	10	9	9	9	10	10	9	10	10	10	10	10	10	10	10	10	10
US-10-125-852-25	09-89	US-09-894-912A-34	US-09-894-912A-10	US-10-125-852-23	US-09-816-028A-39	US-09-894-912A-26		US-10-185-770-4	US-09-867-550-2038	US-10-118-513A-12	US-10-118-513A-8	US-10-118-513A-2	US-09-822-682-2	US-09-919-770-4	US-10-060-036-171	US-09-919-603-2	US-09-821-839-2	US-09-925-301-1031	US-09-872-523-3	us-09-930-871-12	US-09-930-871-2	-93	US-09-930-871-4	US-09-930-871-16	US-09-930-871-6
25,	13,	34,	Sequence 10, Appl	23,	e 39,	26,	16	4, Appl	e 20	12		'n	Ν	(D 4 A	171,	'n	Sequence 2, Appli	Sequence 1031, Ap	ω	12,	2, A	14	Sequence 4, Appli	Sequence 16, Appl	Sequence 6, Appli

ALIGNMENTS

RESULT 1 US-10-068-564-16

; Sequence 16, Application US/100; Publication No. US20030040096A1; GENERAL INFORMATION:

Application US/10068564

SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 16

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
TILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78

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GENERAL INFORMATION:
, APPLICANT: Alnemri, Emad S.
, APPLICANT: Fernandez-Alnemri, Teresa
, TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
, TITLE OF INVENTION: AND METHODS OF USE
                                                                                                       ; Sequence 16, Application US/09989903
; Patent No. US20020146804A1
                                                                                                                                           RESULT 2
US-09-989-903-16
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-16
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                     82 EQLSLQFSNDEDD 94
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                                                                                                                                                                                                                                                                                                                   44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                      95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 75.5; DI 35.6%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
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                                                                                                                                           US-09-815-242-11522
; Sequence 11522, Application US/09815242
; Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-833-790-252
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 252
LENGTH: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 252, Application US/09833790 Patent No. US20020068288A1 GENERAL INFORMATION:
                                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989,903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lodes, Michael J. APPLICANT: Wang, Tongtong
                                                       APPLICANT:
                                                                      APPLICANT:
                                                                                           APPLICANT:
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                                        APPLICANT:
   APPLICANT:
                   APPLICANT:
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                                                                                                                                                                                                                                                                                            45 FEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                               30 EEQEKLLKKSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMKKTA--CGFCFVE 87
                                                                                                                                                                                                                                                                                                                                                                     1 EERE-----DCWTFYANRKYTDFDKS----FKKSSD------LDECKKTCFKTEYCYIV 44
                                                                                                                                                                                                                                                        YYSRADAENAMRYINGTRLDDR--IIRTDWDAGFK---EGRQYGRGRSGGQVRDEYRQD 141
                                                                                                                                                                                                                                                                                                                                                                                                        26;
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Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mohamath, Raodoh
Indirias, Carol Y.
                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
Yamamoto, Robert T
                 Carr, Grant J.
                                      Trawick, John D.
                                                       Wall,
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
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Pred. No. 1.5;
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US-09-815-242-11522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-765-272-200
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11522
LENGIH: 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 200, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 DKTEQSSNDPKEAQKTLFDA----ILLQDLAN--AVYNVMPTK-----LGDRNYWENF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 LTDCEGKDAGNAAGTGDE 96
                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                    APPLICATION NUMBER: 08/961,083
FILING DATE: CIDAROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi et. al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu, H. Howard
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US-09-953-280-46
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-993-999-7
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                                                                                                                                                                                       Sequence 46, Application US/09953280 Publication No. US20030073072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 7
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                                                                                    APPLICANT: Havenga, Menzo
APPLICANT: Vogels, Ronald
APPLICANT: Bout, Abraham
TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
FILE REFERENCE: 2183-4123US
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Best Local
                CURRENT APPLICATION NUMBER: US/09/953,280 CURRENT FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: US 09/348,354 PRIOR FILING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Austen, K. Frank
APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/246,316
PRIOR FILING DATE: 2000-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/993,999 CURRENT FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 WIKQLNKRLEKFD-----SEIINCRVTSEQISCYKSDISYTVF-----LRYFIADFV 368
                                                                                                                                                                                                                                                                                                                      62 DLDRC---CQTHDHCY------SQAKKLESCKFLIDNPYTNTYSYSCSGSE 103
                                                                                                                                                                                                                                                                                                                                                        27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ELDQEKF-----VVDENFTENYLTDCEG-----KDAGNAAGTGDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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o. US20020110891A1
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STRANDEDNESS: single
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(301) 309-8512
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25.0%;
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23.6%; Pred. No. 30;
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                                                                                                                                                                                                                                                             Sequence 1327, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/09801574 Patent No. US20020081592A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                         APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: pF523
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Best Local Similarity
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                    PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING JOHE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR TIPLICATION NUMBER: 60/261,557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Reproduction-Specific Genes FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Peijing Jeremy APPLICANT: Page, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                  1400 NE-----TNVTENYELDV-----ASGTEED 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1349 SSKSYLDKQRILTVDSFAASSTVPHCEQSCREKELLKTEQC-----SSGNCLH--TDG 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 EKGGQAKFIIGDNGQPTENHDITMAFDTPGGTITGGTGGPQDELKAD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ANRKYTDFDK-----SFKKSSDLDECKKTC-----FKTEYCYIVFEDTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 EENQETFVFYGGR-----ALKKET-----KMKPCYGSFARPTN-
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APPLICATION NUMBER: 60/277,379
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Pred. No. 72;
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US-09-974-298-114
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 3267030CD1
US-09-974-298-114
                                                                                                                                                                                                                                       US-09-975-456B-5
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SEQ ID NO 1327
LENGTH: 257
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NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 114
LENGTH: 1125
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                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                          Sequence 5, Application US/09975456B Publication No. US20030073087A1
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CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/239,491
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CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                                       APPLICANT: LAMBEAU, GERARD APPLICANT: LAMBEAU, GERARD APPLICANT: VALENTIN, EMMANUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-10-04 PRIOR APPLICATION NUMBER: 60/238,331
                                                                 TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2 FILE REFERENCE: 1478-R-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                           1076 EEVEEAENEGEEAKTEGLMKDDRAESQASSLGQKVGESSEQVSEE 1120
                                                                                                                                                                                                                                                                                                                                                                                                                1032 EEDED-----SEKEEEEEDKEMEELQEEKECEKPQGDEE-----EEEEEEE-----VEE 1075
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                                                                                                                                                                                                                                                                                                                                                                   61 EELDQEKFVVDENFTENYLTDCEGKDAGNAAG--TGDESDEVDED 103
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nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDES 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 TYYRSKWYNDYAVSVKSRITINPDTSKNQFSLKLSSVTAADTAVYYCARERPYYDILTGY 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EEREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDG 60
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39;
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SOFTWARE: Pat SEQ ID NO 695 LENGTH: 460

PatentIn Ver.

PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-975-456B-5
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US-10-102-806-695
GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 511

    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

                                                                                                                                                                  Sequence 695, Application US/10102806 Publication No. US20030054421A1
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Best Local
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                        68 VDELDKCCQTHDNCY----DQAKK------LDSCKFLLDNPYTHTYSYSCSG
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Local Similarity 29.8%;
es 17; Conservation
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29.8%;
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Pred. No. 18;
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Pred. No. 19
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US-10-092-219-8
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; LICATION: all Xaa positions
; OTHER INFORMATION: Xaa-unknown amino acid residue
US-10-042-417-52
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENCTON
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                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Domin, Jan
                                                                                                                                                                                                                                Sequence 8, Application US/10092219
Patent No. US20020115114A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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11.2%; Score 64; DB
Best Local Similarity 27.1%; Pred. No. 96;
PRIOR APPLICATION NUMBER: PCT/GB98/00244
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/355,160
PRIOR FILING DATE: 1999-10-01
                                                                                        TITLE OF INVENTION: No. US20020115114A1e1 Lipid Kinase FILE REFERENCE: 1064Hg/50947 CURRENT APPLICATION NUMBER: US/10/092,219 CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/042,417 CURRENT FILING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: 60/260,179 PRIOR FILING DATE: 2001-01-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pagano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 590
                                                                                                                                                                                                                                                                                                                                                                    313 VSSENFTSPYVWMLDAEDLADIEDT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 TSHQSGFLKTS-TSKITSTAWKNK--DITMQSTKQYACLHDLTNKGIGEEIDNEHPWTKP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 ASDDEHDEHDEN 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 REDLHILFSNHGEIKWIDFVRGAKEGIILFKEKAKEALGKAKDANNGNLQLRNKEVTWEV 357
                                                                                                                                                                                                                                                                                                                                                                                                                    69 VVDENFTENYLTDCEGKDAGNAAGT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 TDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVD---GEELDQE----KF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 --- DESDEVDED 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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Search completed: May Job time: 36 secs
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PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 294
                                                                                                                                                                                                 Query Match
Best Local Similarity 28.8
Matches 19; Conservative
                                                                   104 LLDDNF 109
                                                                                                   69 VVDENF 74
                                                                                                                                       45 DRQMTDSPRGFELSSSTRQRTQGFNKQDYDLMVFPELDSQKRAVD-IDVEKLTQAELEKI 103
                                                                                                                                                                   12 NRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ---EKF 68
               5, 2003, 17:54:15
                                                                                                                                                                                                   11.0%; Score 63; DB 28.8%; Pred. No. 55; tive 18; Mismatches
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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: мау 5, 2003, 17:48:57 ; Search time 36 Seconds

(without alignments)
275.051 Million cell updates/sec

Perfect score: Title: US-09-936-737A-2 573 1 EEREDCWTFYANRK

EEREDCWTFYANRKYTDFDK.....GKDAGNAAGTGDESDEVDED 103

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

Database : PIR_73:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ر ت	4	ω	2	ш	No.	Result	
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12.3	12.3	٠	•	12.3	٠		•	12.6	•	12.7	12.7	12.7	12.7		12.9	•		13.0	•	•	13.2	13.2	•	٠	13.7	•	14.0	14.0	Match	Query	٥
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T18444 T26487 D70100	T32824 T33328 T28317	D95206 AI3625	B97104 PSPGA T37899	C86406 T24432 S50295 F71909
hypothetical prote hypothetical prote phosphoglucomutase	hypothetical prote hypothetical prote ORF MSV156 hypothe	nypothetical prote hypothetical prote ribonucleoside-dip	hypothetical prote phospholipase A2 (hypothetical prote	88.6K hypothetical hypothetical prote hypothetical prote hypothetical prote

ALIGNMENTS

leech antiplatelet protein precursor - Mexican leech C;Species: Haementeria officinalis (Mexican leech) C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-May-1999 C;Accession: A42435; A42434

R;Keller, P.M.; Schultz, L.D.; Condra, C.; Karczewski, J.; Connolly, T.M. J. Biol. Chem. 267, 6899-6904, 1992
A;Title: An inhibitor of collagen-stimulated platelet activation from the salivary gla;Reference number: A42435; MUID:92202247; PMID:1551898
A;Accession: A42435.

A; Molecule type: mRNA A; Residues: 1-147 <KEL>

for residu

A;Cross-references: GB:M81489
A;Note: the authors translated the codon AGC for residue 20 as Arg and GAA
A;Note: the authors translated is shown at residue 65
A;Note: sequence extracted from NCBI backbone (NCBIN:91615) and modified
R;Connolly, T.M.; Jacobs, J.W.; Condra, C.
J. Biol. Chem. 267, 6893-6898, 1992
A;Title: An inhibitor of collagen-stimulated platelet activation from the s
A;Reference number: A42434; MUID:92202246; PMID:1551897 salivary gl

A; Accession: A42434

A; Molecule type: protein A; Residues: 59-91; 101-113; 123-139 <CON>

F;22-147/Product: leech antiplatelet protein #status predicted <MAT> F;1-21/Domain: signal sequence #status predicted <SIG>

Query Match Match 14.0%; Score 80.5; DB 2; Local Similarity 32.7%; Pred. No. 1.7; Conservative 10; Mismatches 24; Length 147; Indels з ; Gaps

1,

В QУ 66 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRN 120 5 DCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEY---CYIVFEDTVNKECYYN 56

RESULT 2 A55320

immunophilin FKBP46 - fall armyworm

C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 02-Sep-2000
C;Accession: A55320

R;Alnemri, E.S.; Fernandes-Alnemri, T.; Pomerenke, K.; Robertson, N.M.; Dudley, K.; D J. Biol. Chem. 269, 30828-30834, 1994
A;Title: FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms a protein-ki
A;Reference number: A55320; MUID:95074110; PMID:7527037

A; Reference number: A55320; A; Accession: A55320

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-412 <ALN>

A;Cross-references: GB:U15038; NID:g595844; PID:g595845 C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomeras

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hypothetical protein Y69H2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                            A;Map position: 5
A;Introns: 23/3; 65/1; 105/1; 146/1; 191/1; 241/1; 293/1; 381/1; 419/1; 461/1; 499/1; 55
                                                                                                                                                                                                                A; Experimental source: clone Y69H2 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: Z20234
A;Accession: T26562
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F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPT>
                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-907 <WILL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 134/3; 160/1; 286/3; 316/1; 480/2; 502/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL;AL110478; NID:e1542139; PIDN:CAB54340.1; CESP:Y26D4A.2
A;Experimental source: clone Y26D4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-550 <WIL>
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                                                                                                                                                                                          A; Gene: CESP: Y69H2.2
                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z98877; PIDN:CAB11570.1; GSPDB:GN00023; CESP:Y69H2.2
                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z20343
A; Accession: T27317
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;McMurray, A.
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Matches
                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 DE--NDESFKMN--TSAEGDDSDEEDDDDEDEEDEEDDD
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  10 YANRKYTDFDKSFK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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33; Conser
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                                                                     13.7%;
29.2%;
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---KSSDL------DECKKTC--FKTEYGYIVFEDT
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                                                                     Score 78.5; DB Pred. No. 16;
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DKSFKKS-SDLDECKKTCFKTEYCYI 43
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                                                                                                                                                                                                                                                                J. Virol. 66, 5047-5058, 1992
A;Title: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A37309; MUID:92333688; PMID:1321287
A;Contents: annotation; protein-coding frames
A;Contents: annotation; protein-coding frames
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84021
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-797 < ALB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus
A;Reference number: A36806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06689.1; GSPDB:A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-682 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A36811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Albrecht,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ORF48 - saimiriine herpesvirus 1 (strain 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
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                                                                                                                                           Query Match
Best Local :
                                                                                                                    Matches
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                      382 ANEK--EYKKIIDKSDDRDDRDKDEYELE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 EELEEEKF -- DERFLVTLLTKVDGEE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 YDEFEMTVLDQSFEQGYQAYQIEVTLDE--KTLLKAARVFMVFEVLEQVG-EVIKSTPSA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 VNSRCI--VYEAGEME-----TDPNACEDNSTLC-GAELGHGMCINWQSDVTD 324
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                                                                11 ANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYN----VVDGEELDQE 66
                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 YANRKYTDFDKSFKKSSD------LDECKKTCFKTEYCYIVFE--DTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAQEKSTD-DKTLKYLTLCGEWCMVSEDMLVKDDVSMKDDCKKSCGGDSSEYC----GK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD 101
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                                                                                                                                           Similarity
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                                                                                                                                        13.6%;
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                                                                                                               12;
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Pred. No.
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                                                                                                                                           DB 2;
16;
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                        NEE--YNRDEEEDEGEDEEDE 427
                                                                                                                    33;
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                                                                                                                                                               Length 797;
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PID:g60369

B.; Newman,

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A.Description: The sequence of C. elegans cosmin rada, Reference number: Z18498
A.Recession: T16334
A.Recession: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
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T16354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F42G9.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16354
R;Taich, A.
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A;Introns: 37/3; 254/2; 364/2; 406/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1996 A; Description: The sequence of C. elegans cosm
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C;Accession: T22054
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A;Cross-references: EMBL;Z77661; PIDN:CAB01183.1; GSPDB:GN00023; CESP:F40G12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z19507
A; Accession: T22054
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F40G12.5 - Caenorhabditis elegans
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Best Local
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                                                                                                                                                                    10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEK 67
                                                                                                                                                                                                                                 Local Similarity
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                                                        DIGDEG --
                                                                                         FVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD 101
                                                                                                                              FTSAKLPDFLKERKFWEADDVAECLQKAF-----VDFDDFIRAE---
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                                                    --KPKKAGGEADSEDEADRID 137
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                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                               Score 75.5;
Pred. No. 1
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                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                              PID:g1216310; PIDN:AAA91358.1; CESP:F42G9
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RESULT 11
T32731
PAR interacting protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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C;Genetics:
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Infect. Immun. 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: aarpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-3844 <B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Barale, J.C.; Candelle, D.; Attal-Bonnefoy, G.; Dehoux, P.; Bonnefoy, S.; Ridley, R Infect. Immun. 65, 3003-3010, 1997
A;Title: Plasmodium falciparum AARP1, a giant protein containing repeated motifs rich A;Reference number: Z18929; MUID:97378065; PMID:9234746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asparagine/aspartate rich protein - malaria parasite (Plasmodium falciparum) (fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T18402
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C; Superfamily: Caenorhabditis elegans hypothetical protein ZK1290.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U21308; PIDN:AAB93316.1; GSPDB:GN00020; CESP:ZK1290.10 A;EXperimental source: strain Bristol N2; clone ZK1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-360 <TAI>
A; Cross-references: EMB
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A; Accession: T34510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK1290.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000 C;Accession: T34510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                        1726 EDSEECQIKESYKKMSECNNKENIIFDSISVLRKNNIKRLKNYMCKNKNCYIYYDDNNNK 1785
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                                                                                                                                                                                                                                                                                                                     1 EEREDCWTFYANRKYTD------FDK-SFKKSSDLDECKKTCFKTEYCYIVFEDTVNK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-3844 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                                                                                                                                              13.1%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 2;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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R;Comte, P.A.; Ossipow, V.; Schibler, U. submitted to the EMBL Data Library, January 1997

29-Oct-1999

C; Accession: T32731

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A; Gene:
C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein aq_1923 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: Isolation of PIP, a
A;Reference number: Z21213
A;Accession: T32731
A;Status: preliminary; translated
                                                                           Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, A;Title: Genomic sequence of a Lyme disease spirochaete, A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70236
                                                                                                                                                                                                                                           hypothetical protein BBH09 - Lyme disease spirochete plasmid H/lp28-3 c;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 c;Accession: B70336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70465
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A;Residues: 1-1277 <COM>
A;Cross-references: EMBL:U83590; NID:g2253210; PID:g2253211; PIDN:AAB62878
                                   A; Molecule type: DNA
                                                                                                                                                                                                                  R; Fraser,
                                                                                                                                                                                                                                       C; Accession: B702
                                                                                                                                                                                                                                                                                                                        B70236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D70465
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    A;Cross-references:
                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-296 < AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown;
                                                        A;Status:
                                                                                                                                                                                 Bowman,
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Best Local :
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                                                                                                                                                        aser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; wman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, re 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671 GEESEEEDRDKDVDPGFRQQLM---EVLQAGNALGGEEEEEE 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GEELDQE--KFYVDENFTENYLTDCEGKDAGNAAGTGDESDE
                                                                                                                                                                                                                                                                                                                                                                                                          68 YRDRNGEEFKIEEIIIEK-----LSETEGK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _aq_1923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFAYDKYMDNKAKEQVEYFLDKTLRKSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYANRKYTD-----FDKSFKKSSDLDECKKTCFKTEYCYIVFE----DTVNKECY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDEED-----NVVVTDTDEKQLKHGEDADSDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                             YNVVDGEELDQEKFVVDENFTENYLTDCEGK
                                                        preliminary; nucleic acid sequence not shown;
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                    1-1278 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aquifex aeolicus hypothetical protein aq_1923
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  GB:AE000784;
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30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 74; DB 2; Length 296; 24.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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Pred. No. 53;
9; Mismatches
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  NID: g2690041; PIDN: AAC66000.1; PID: g2690056; TIGR: BBH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from GB/EMBL/DDBJ
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                                                                                                                    Borrelia burgdorferi
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hypothetical protein F26F2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Caccession: T21428 R;Ainscough, R. Submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Genome: plasmid
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F;2139/Binding site: ATP
F;2466/Binding site: ATP
F;2811/Binding site: ATP
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A; Residues: 1-4466 <OGA>
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                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                        EEREDCWTFYANRKY-----
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                                                            #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                   Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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A, Molecule type: mRNA
A, Molecule type: mRNA
A; Residues: 764-1001. 'APQ',1005-2036, 'VPSSVET' <0G2>
C; Superfamily: dynein heavy chain, ciliary
C; Keywords: ATP; heterotetramer; hydrolase; microtubule |
F; 154-161/Region: nucleotide-binding motif A (P-loop)
F; 1852-1859/Region: nucleotide-binding motif A (P-loop)
F; 2133-2140/Region: nucleotide-binding motif A (P-loop)
F; 2460-2467/Region: nucleotide-binding motif A (P-loop)
F; 2805-2812/Region: nucleotide-binding motif A (P-loop)
F; 160/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 352, 643-645, 1991
A,Title: Four ATP-binding sites in the midregion of the beta heavy chain of dynein.
A,Reference number: S17231; MUID:91326104; PMID:1830928
A,Accession: S17231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Anthocidaris crassispina
C;Date: 30-Sep-1991 #sequence_revision 02-May-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: ATP-binding site in dynein beta-heavy chain: identification by molecular clo A; Reference number: PS0415
A; Accession: PS0415
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                                                                                                                                        EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
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                                                                    Herpesvirus saimiri (strain 11)
                                                                                                                       Hypothetical gene
                  Gammaherpesvirinae;
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J. Biol. Chem. 269:30828-30834 (1994).

I. FUNCTION: BINDS TO, AND IS INHIBITED BY FK506 AND RAPAMYCIN. BIND DOUBLE-STRANDED DNA IN VITRO. PPLASES ACCELERATE PROTEIN FOLDING.

I. CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

I. SUBCELLULAR LOCATION: Nuclear.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; G
Ditrysia; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95074110; PubMed=7527037;
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ASP/GLU-RICH (HIGHLY ACIDIC).
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       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;
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01-NOV-1997
                                                                                                                                                                                                         FEBS Lett. 403:61-69(1997).
                                                                                                                                                                                                                                                                      van
                                                                                                                                                                                                                                                                              MEDLINE-97190206; PubMed-9038361; van de Craen M., Vandenabeele P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-12 precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                        Fiers W.;
                                                                                                                                                                                                                                                                                                                    STRAIN=C3H/An;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                           CASP1
                                                                                                                                                                                                                                    "Characterization of seven murine caspase family members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICEC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X64346; CAA45671.1; -. PIR; A36811; A36811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92333688; PubMed=1321287; Albrecht J.-C., Nicholas J., Biller D Newman C., Wittmann S., Craxton M.A., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   G., Molemans F., Schotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 AA; 8
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. 35, Last sequ
. 41, Last anno
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biller D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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P., van Criekinge
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oleman H., Fleckenstein I
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Best Local Similarity
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SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE: PS01029; CARD; 1.
PROSITE: PS01122; CASPASE_LCYS; 1.
PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS01121; CASPASE_P10; 1.
PROSITE: PS05200; CASPASE_P10; 1.
PROSITE: PS05200; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                P2C1_CAEEL STANDARD; PRT; 491 AA. P49595; O1-FEB-1996 (Rel. 33, Created) O1-OCTT-1996 (Rel. 34, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update) Probable protein phosphatase 2C F42G9.1 (EC 3.1.3.16) (PP2C).
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                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAEEL
EMBL; U00051; AAA91358.1;
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                 STRAIN-Bristol N2;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
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CHAIN
                                                                                                                                      phosphate.
-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                   Taich A.,
                                                                                                                                                                               -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Thiol protease; Apoptosis; Zymogen.
PROPEP 1 ? POTENTIAL.
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Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002398; ICE_p10.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y13090; CAA73532.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 VFEDTVNKECYYNYVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 DE----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                Waterston R.;
1 (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 AA;
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35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75.5;
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Best Local S
Matches 23
                                                                                                                         Query Match
                                                                                                                   Matches
                                                                                                                                                                                                                                                                             SMART; SM00254; ShKT; 1.

Hypothetical protein; Signal.

SIGNAL 1 21
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                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003582; ShKT.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U21308; AAB93316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadore; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann
Hypothetical 39.7 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOFA_CAEEL
Q09337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
METAL
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SMART; SM0033; PP2CC; 1.

PROSSITE; PS01032; PP2C; 1.

Hypothetical protein; Hydrolase; Magnesium; Manganese.

METAL 37

MANGANESE 1 (BY SIMILARIT METAL 38 38

MANGANESE 1 (BY SIMILARIT METAL 37

MANGANESE 1 (BY SIMILARIT METAL 38 38)

MANGANESE 1 AND 2 (BY SIM
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Wormbep; F4269.1; CE07231.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                           WormPep; ZK1290.10; CE02080.
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224 EDTYGEE----NVFDFDKLFDKKIYIRNDGSTTENTTEQSTTEKTGTKKGTIEVSVELGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 DIGDEG-----KPKKAGGEADSEDEADRID 137
                                                    46 EDTVNKECYYNVVDGEELDQEKFVV-----DENFTENYLTDCEGKDAGN-----AAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEK 67
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                                                                                                                                                                                                                            360 AA;
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea;
                                                                                                                                                                                                                            39669 MW;
                                                                                                                                           13.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
protein ZK1290.10 in chromosome II precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                           Score 75; DB 1; Length 360, Pred. No. 4.8; 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANGANESE
MANGANESE
MANGANESE
                                                                                                                                                                                                                         HYPOTHETICAL PROTEIN ZK1290.10; 18751B6BC062D4F7 CRC64;
                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILA
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
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RESULT 8
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-AAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, ciliary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hypothetical protein AQ_1923 precursor.
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                                                                                                                                                                                                                                                                                                  Anthocidaris crassispina (Sea urchin)
Eukaryota; Metazoa; Echinodermata; Ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                  Echinoidea;
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                                                 MEDLINE=91326104; PubMed=1830928;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=7629;
                                                                                                                                                                                                                          Anthocidaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRDRNGEEFKIEEIIIEK-----LSETEGK 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYANRKYTD-----FDKSFKKSSDLDECKKTCFKTEYCYIVFE----DTVNKECY 54
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34566 MW;
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24.2%;
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                                                                                                                                                                                                                                                                  Echinacea; Echinoida;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 352:643-645(1991).
-I- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dynein.
                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase alpha catalytic subunit (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Four ATP-binding sites in the midregion of the beta heavy chain
                                                                                                                                                                                 DPOA_SCHPO
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Damagnez
        SEQUENCE FROM N.A. MEDLINE=91238692;
                                                         Schizosaccharomyces.
                                                                                                                                                                        P28040;
                                            NCBI_TaxID=4896
                                                                                                     POL1 OR SWI7 OR SPAC3H5.06C
                                                                                                                                                                                                                                          520 FKMLDCYGPLLDRPVIRNDF---ECKYPIVLMLYDQELDQSKEIYDEH 564
                                                                                                                                                                                                                                                                                      460 EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
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                                                                                                                                                                                                                                                                FKTEYCY-----IVFEDTVNKECYYNVV---DGEELDQEKFVVDEN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Microtubules; Dynein; ATP-binding; Flagella;
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           PubMed=2034212;
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  de Recondo A.-M., Baldacci G.;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                     14;
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Pred. No. 81;
14; Mismatches
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RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Vonstreels E., Rleger M., Schaefer M., Mueller-Auer S.,
RA Woodward J., Vonstreels E., Rleger M., Schaefer M., Mueller-Auer S.,
RA Woodward J., Vanstreels E., Rleger M., Schaefer M., Mueller-Auer S.,
RA Woodward J., Vanstreels E., Rleger M., Boahardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002)
Nature 415:871-880(2002)
       TIGREAMS; TIGR00592; pol2; 1.
PROSTIE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holloyd S., Hornsby T., Howarth S., Huckle E.J., Hut S., Jagels K.,
                                                                                             PRINTS; PR00106; DNAPOLB SMART; SM00486; POLBC; 1
                                                                                                                                            Pfam; PF00136; DNA_pol_B; 1. Pfam; PF03104; DNA_pol_B_exo;
                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS A REPLICATIVE POLYMERASE.
-1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                             InterPro; IPR002064; DNA_pol_B.
InterPro; IPR004578; Pol2.
                                                                                                                                                                                                                                         PIR; S15993; DJZPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93140876; PubMed=8423854; Jagmohan S., Klar A.J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The POL1 gene from the fission yeast, Schizosaccharomyces pombe, shows conserved amino acid blocks specific for eukaryotic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA polymerase-alpha is essential for mating-type switching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerases alpha."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULÁR LOCATION: Nuclear.
MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALDHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIFFERENT REACTIONS OF DNA SYNTHESIS.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                             X58299; CAA41232.1; -.
X69673; CAB57881.1; -.
Z99296; CAB16598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DNA) (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast."
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Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             institutions as long as its content
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RESULT 10
YVV2_Y
AC P40157
DT 10-FEB
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DT 01-FEB
DT 01-FEB
CO NCBL-1
RN 1012012
Saccha
OC .Eukary
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OX NCBL-1
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RD STRAII
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           RESULT 11
MOH1_CANPG
ID MOH1_C
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Best Local
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P40157;
01-FEB-1995
P81034;
15-JUL-1998 (Rel. 36, Created)
                                                                 MOH1_CANPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 271488; CAA96114.
SGD; S0005156; YNL212W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coster F., van Dyck L., Jonniaux J.-L., Purnelle B., Goffeau A.; "The sequence of a 13.5 kb DNA segment from the left arm of yeast chromosome XIV reveals MERI; RAPI; a new putative member of the DNA replication complex and a new putative serine/threonine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Hypothetical 88.8 kDa protein in PEXI7-MERI intergenic region.
YNLZ12W OR N1327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 11:85-91(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288c / FY1679;
MEDLINE=95282517; PubMed=7762305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                    315
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                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                    24 KSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEE---LDQEKFVVDENFTENYLT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
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Z71488;
                                                                                                                                                                                                                                                            DCEGKDAGNAAGTGDESDEVDED
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                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO C.CARDUNCULUS PROTEIN CYPRO4 AND S.POMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88845 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%; Score 71;
26.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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Pred. No.
                                                                                                                                                                                                                                                            103
                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCBB1F4CE32BF97C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 782
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P06596;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 precursor (EC 3.1.1.4) (Phospholipase) (Group IB phospholipase A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the crab, carce regered the growth and reproduction.";

J. Biol. Chem. 271:12749-12754(1996).

-I- FUNCTION: REPRESSES THE SYNTHESIS OF METHYL FARNESOATE, THE
PRECURSOR OF INSECT JUVENILE HORMONE III IN THE MANDIBULAR ORGAN.

-I- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN

-I- TISSUE SPECIFICITY: PRODUCED BY THE SINUS GLAND WHERE IT IS
gene.
Eur.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer pagurus (Rock crab).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Cancroidea; Cancridae; Cancer
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15-JUN-2002 (Rel. 41, Last annotation update)
Mandibular organ-inhibiting hormone-1 (MOIH-1).
                                                                 SEQUENCE FROM N.A.
MEDLINE=90306027; PubMed=2142076;
METFALEC B., Laforge K.S., Vasiloudes
"Isolation and sequence of the canine
                                                                                                                                                                                                                          sequences
                                                                                                                                                                                                                                                    "Dog
                                                                                                                                                                                                                                                                          Ohara O., Tamaki M., Na
Teraoka H., Okamoto M.;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-86223862;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01147; Crust_neurohorm; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Sinus gland;
MEDLINE-96278659; F
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SIMILARITY: BELONGS TO THE ARTHROPOD
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                          Biochem.
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                                                                                                                                                                                                rat pancreatic phospholipases A2: s deduced from complementary DNAs. em. 99:733-739(1986).
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                          190:299-304(1990)
                                                                                                                                                                                                                                                                                                 PubMed=3754861;
M., Nakamura E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TDFDKSFKKSSDLDECKKTCF-KTEY--CYIVFEDTVNKE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Canidae;
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8DB338A39058A62D CRC64;
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                                                                       P., Puigserver A., Scheele G.A.; pancreatic phospholipase A2
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Best Local S
Matches 15
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EMBL; M35301; AAA3088;
PIR; A24392; PSDG.
PIR; S11316; S11316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                  P52298; Q14924;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
20 kDa nuclear cap binding protein (NCBP 20 k
                                                                                                                                                                                                                                                                                                                                                                                               CA_BIND
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-I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.
-I- COPACTOR: Binds 1 calcium ion per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87175472; PubMed=3562437;
Kerfelec B., Laforge K.S., Puigserver A., Scheele G.
"Primary structures of canine pancreatic lipase and
messenger RNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pancreas 1:430-437(1986).
                 interacting protein 1) (NIPI).
NCBP2 OR CBP20.
                                                                                                                                                CB20_HUMAN
                                                                                                                                                                   HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00389; PHPHLIPASEA2. ProDom; PD000303; PhospholipaseA2;
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SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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15; Conserv
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VIA CARBO
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No. 4
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phospholipase A2
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 Q58285;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Nuclear protein; RNA_binding.
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Genew; HGNC:7659; NCBP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN MEDIATING U SNRNA EXPORT FROM THE NUCLEUS BINDS TO 5'CAPPED MRNA.
-I- SUBUNIT: THE CAP-BINDING PROTEIN (CBC) COMPLEX IS AN HETERODIMER OF CBP80 AND CBP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kataoka N., Ohno M., Moda I., Shimura Y.;
"Identification of the factors that interact with NCBP, an nuclear cap binding protein.";
nucleic Acids Res. 23:3638-3641(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                Piam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X84157; CAA58962.1; -. EMBL; D59253; BAA09599.1; -.
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McGuigan C., Mattaj A.W.;
"A cap-binding protein complex mediating U snRNA export.";
Nature 376:709-712(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cervix;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                        88 YYSRADAENAMRYINGTRLDDR--IIRTDWDAGFK---EGRQYGRGRSGGQVRDEYRQD 141
                                                                                                                                                       45 FEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                             30
                                                                                                                                                                                                                        1 EERE-----DCWTFYANRKYTDFDKS----FKKSSD------LDECKKTCFKTEYCYIV 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                               METJA
                                                                                                                                                                                        EEQEKLLKKSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMKKTA--CGFCFVE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                605133;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00076
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                      156 AA; 18001 MW;
 (Rel.
                                                                                                                                                                                                                                                         Conservative
                                               STANDARD;
 36, Created)
                                                                                                                                                                                                                                                                         21.8%;
                                                                                                                                                                                                                                                                                      12.3%;
sequence update)
                                                                                                                                                                                                                                                         20;
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                                                                                                                                                                                                                                                                       Score 70.5; DB 1; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                    B6C94F3182A2CC3D CRC64;
                                               PRT;
                                                                                                                                                                                                                                                                                                                                        v
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                   (IN REF.
                                               748 AA
                                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                       23;
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RESULT 15
S185_YEAST
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Best Local
                                                                                                                                                                                                                                                        S185_YEAST STANDARD; PRT; 1058 AA. P40856; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) SIT4-associating protein SAP185 OR YJL098W OR J0840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JALI / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-6688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                  Mol. Cell.
                                                                                   "The SAP,
                                                                                                       Arndt
                                                                                                                      MEDLINE=96220458; PubMed=8649382; Luke M.M., della Seta F., di Como
                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome. SEQUENCE 748 AA; 90731 MW; 5515ED3B541562EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
            SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67531; AAB98882.1; -.
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                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2190;
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                                                                  the SIT4 phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                               a new family of proteins,
                                                  Biol. 16:2744-2755(1996).
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                                                                                                                      di Como C.J.,
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Pred. No. 27;
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                                                                                   associate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                    Sugimoto H., Kobayashi R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 748;
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                                                                                 function positively
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STRAIN=S288c;

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Search completed: May 5, 2003, 17:49:27 Job time: 24 secs
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Best Local S
Matches 25
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"A 37.5 kb region of yeast chromosome X includes the SMEI, MEFZ, GSHI and CSD3 genes, a TCP-1-related gene, an open reading frame similar to the DAL80 gene, and a tRNA(Arg).";

Yeast 11:873-883(1995).

-I- FUNCTION: ASSOCIATES WITH THE SIT4 PHOSPHATASE IN A CELL CYCLE DEPENDENT MANURE. MAY BE DIRECTLY OR INDIRECTLY INVOLVED IN SIT4-DEPENDENT FUNCTIONS IN BUDDING AND IN NORMAL G1 CYCLIN
                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; Cell cycle. SEQUENCE 1058 AA; 121402 MW; DD44DD53DDD87438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X77923; CAA54892.1; -.
EMBL; X85021; CAA59396.1; -.
EMBL; Z49373; CAA89392.1; -.
SGD; S0003634; SAP185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288c / FY1679;
MEDLINE-96090136; PubMed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisiae chromosome X including the BCK1 gene."; Yeast 10:1481-1488(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- PTM: HYPERPHOSPHORYLATED IN THE ABSENCE OF SIT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-853 FROM N.A. STRAIN-S288C / FY1679;
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miosga T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zimmermann F.K.;
                                                                                542 EDD 544
                                                                                                                                                            485 HCSNMTLLNEPSAYDIVRERDAERERIFNSQNYVDSNDRSELKENEDDN---TGDADDEV 541
                                                                                                                                                                                                                                          427 DRDPIYLGYLVKMFSEHMADFNKI--LIEKKIPLLQTSYGTIEPLGFERFKICELIAELL 484
                                                                                                                                                                                 47 -----DTVNKECYYNVVDGEELDQEKFVVDENFTE-NYLTDCEGKDAGNAAGTGDESDEV 100
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                                                                                                                                                                                                                                                                                EREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEY-------CYIVFE-- 46
                                                                                                                                                                                                                                                                                                                          ch 12.2%; Score 70; DB 1; Length 1058; Similarity 20.3%; Pred. No. 43; 25; Conservative 27; Mismatches 45; Indels :
                                                                                                                                                                                                                                                                                                                      26; Gaps
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: sp_archea:*
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573
1 EEREDCWTFYANRK
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_archeap:*
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Q9X9S1
Q9U2Q4
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050667
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035821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580
                                                        Q9k8n5 bacillus ha
097239 plasmodium
Q9vfh8 drosophila
Q8syg5 drosophila
Q8syg5 drosophila
Q03650 trypanosoma
Q20246 caenorhabdi
Q94648 plasmodium
                                                                                                                                               Q8xj41 clostridium
Q9x9s1 streptococc
Q9u2q4 caenorhabdi
Q9xts9 caenorhabdi
         Q9fiw8 arabidopsis
035821 rattus norv
Q9fk41 arabidopsis
050667 borrelia bu
                                                                                                                                                                                                               Description
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Q9nex0 caenorhabdi	Q9NEX0	G	1481		70	S
Q97ii6 clostridium	Q97II6	16	1255	12.2	70	4
helicobac	Q9ZLG7	16	1167		70	ω
	Q9SPU5	10	793		70	2
Q9lkr9 arabidopsis	Q9LKR9	10	703		70	Ξ
	88XS8	ر ت	669		70	0
Q94718 paramecium	Q94718	J	521		70	3
Q22144 caenorhabdi	Q22144	ഗ	328		70	æ
9	Q65239	12	292		70	37
Q,	Q8T2M5	ъ	2472		70.5	8
	Q9C7E7	10	786		70.5	5
Q8rhs6 fusobacteri	Q8RHS6	16	600		70.5	4
Q9vir9 drosophila	Q9VIR9	G	367		70.5	Ξ
	Q9D5G6	11	296		70.5	ວັ
Q9ca59 arabidopsis	Q9CA59	10	256		70.5	ũ
ance	Q9U5Y6	ഗ	112		70.5	õ
nomo	Q9H501	4	851		71	9
Q9ha35 homo sapien	Q9HA35	4	589		71	8
⋾	Q9NX93	4	551		71	7
Q9pp61 campylobact	Q9PP61	16	594	12.5	71.5	6
	Q8XHG9	16	540		71.5	5
	096214	ഗ	320		71.5	4
o	Q9SKS0	10	1303		72	ω
P90589 paramecium	P90589	G	2533		72.5	2
	Q27183	ഗ	2533		72.5	12
	001627	σı	564		72.5	õ
	P90649	5	2543		73	9
Q9xv53 caenorhabdi	Q9XV53	ű	643		73	8
Q9v6s9 drosophila	Q9V6S9	5	1154		73.5	7

ALIGNMENTS

RESULT 1 Q8XJ41

08XJ41

PRELIMINARY;

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                                                                                                                                                        Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8XJ41;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                               EMBL; AP003192; BAB81626.1;
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 3.
SMART; SM00028; TPR; 3.
                                                                                                                                                                                                                                      Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anae. flesh-eater."; flesh-eater."; Flesh-eater."; Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                   Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID-1502;
                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical CPE1920.
                                                                                                                                                        Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=13 / TYPE A;
                                                                                                                                                                                                                                                                                                            PubMed=11792842;
36 FKTEYCYIVFEDTVNKECYYNV---VDGEELDQEKFV 69
                                          11
                                                                    10 YANRKYTDFDKSFKKSSDLDECK-----KTC 35
                                                                                                               Local
                                       YNTRNYSDAINYYKKALDNDECKCHSYYNAGYCYIKLKQYEKAIEMITKALELYQDSKYF 70
                                                                                                              Similarity
                                                                                                                                                      11 protein; Complete
116 AA; 13590 MW;
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       protein CPE1920
                                                                                                              13.7%;
22.7%;
                                                                                                                                                    Complete proteome.
3590 MW; 9D6B5D847B3A7312 CRC64;
                                                                                                 11; Mismatches
                                                                                                              Score 78.5;
Pred. No. 1.
                                                                                                              1.9;
                                                                                                                           DB 16;
                                                                                                 27;
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Q9CQ49

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RESOLUTION OF THE PROPERTY OF 
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Best Local S
Matches 23
   Query Match
Best Local S
Matches 23
                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALL10478; CAB54340.1; -
InterPro; IPR001304; Lectin_C.
SMART; SM00024; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9U2Q4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Llull D., Munoz R., Lopez R., Garcia E.;
"A single gene (tts) located outside the cap locus directs the formation of Streptococcus pneumoniae type 37 capsular polysaccharide: type 37 pneumococci are natural, genetically binary strains.";
J. Exp. Med. 19:241-251(1999).
EMBL; AJ131985; CAB51329.1; -.
EMBL; AJ131985; CAB51329.1; -.
Pfam; PF00535; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 509 AA; 58888 MW; C6C38DZACFABOD8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9X9S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9X9S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9U2Q4
                                                                                                                                                                                                                                                                                                                                                                                            none;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y26D4A.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polysaccharide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y26D4A.2
                                                                                                                                                                                                                                                                                                                                                 'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 FETVILDDSKSEVY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 TFYLNNYIHIYGSSFKKSSSISEAKKVILL--YC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVN---KECYYNVVDGEELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEKEVVDENFTENY
       l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                        550 AA;
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                        62195 MW;
                                   13.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.7%; Score 78.5; Di
31.1%; Pred. No. 9.8;
Live 10; Mismatches
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13,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ
   Score 78.5; D
Pred. No. 11;
12; Mismatches
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Last
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                        79AE220EB127466A CRC64;
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annotation
                                                                                                                                                                                                                                                                                                                                                 .elegans:
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                                                                       DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group;
                                                                                                                                                                                                                                                                                                                                                 A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TANDFVPECLVESMQQDYAN 125
   32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 509;
Indels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillales;
   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
   Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 33
                  ul-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Two-component sensor histidine kinase involved in cheat or BH2970.
EAGATING.
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; UNKNOWN_8.
PROSITE; PS01186; EGF_2; 4.
EGF-Like domain; Glycoprotein.
SEQUENCE 907 AA; 101840 MW; 88:
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1078; AMINACHANNEL. PRINTS; PRO0010; EGFBLOOD. SMART; SM00181; EGF; 8.
Bacillus halodurans. Bacteria; Firmicutes;
                                                                                                    Q9K8N5
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561; EGF-like.
InterPro; IPR001438; EGF_II.
InterPro; IPR001873; Na+channe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF000858; ASC; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z98877; CAB11570.1;
HSSP; Q12784; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMurray A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
                                                                                                                                                                280 VNSRCI--YYEAGEME-----TDPNACEDNSTLC-GAELGHGMCINWQSDVTD
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                                                                                                                                                                                                                                 10 YANRKYTDFDKSFK------KSSDL-----DECKKTC--FKTEYCYIVFEDT 48
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                                                                                                                                                                                                                 YAQEKSTD-DKTLKYLTLCGEWCMVSEDMLVKDDVSMKDDCKKSCGGDSSEYC----GK
                                                                                                                                                                                        VNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYYDKDSKECWWWSIDNVHF-LEKVHPSEN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFEDTVNKECYYNVVDGEELDQEKFVVDEN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGNFLHNRPYPDSCETECMDTMVQVNAKPGPLMGSRNIKDNLTSSDECVKYCWKDLNCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWTFYANRKYTDF ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2 protein.
                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                               Similarity
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                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peloderinae;
                                                                                                                                                                                                                                                                            13.7%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_II.
Na+channel_ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ
 Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12,
12,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                        Score 78.5;
                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                    8B55FF139F8F81D7 CRC64;
                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                907
                                                                                                     682
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                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A platform
                                                                                                                                                                                                                                                                   33;
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                                      in chemotaxis
                                                                                                                                                                                                                                                                                           Length 907;
 Bacillales;
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                                                                                                                                                                  324
                                                                                                                                                                                         101
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                097239
                       MEDLINE-99376085; PubMed=10448855;

Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,

Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,

Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horns

Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,

Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,

Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,

Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;

"The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Hypothetical 467.9 kDa protein.
PFC0245C, MAL3P2.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Si
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00260; CheW; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00073; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02518; HATPa
Pfam; PF01627; Hpt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Rés. 28:4317-4331(2000).
-- I- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
EMBL, APO01517; BAB06689.1; --
HSSP; Q56310; 1B3Q.
                                                                                                                                                                                                                          Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
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NCBI_TaxID=86665;
Nature 400:532-538(1999).
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=36329;
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            falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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); IPR004358; Bact_sens_pr_C.
); IPR002545; CheW.
); IPR004105; H-Kinase_dim.
); IPR004359; HIS_KIN_sig.
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32.6%;
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Pred. No.
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., Kuhara S.,
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RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Hilm., Hoskins R.A., Galle R.F., RR Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RR Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RR, R. Haller R.E., Royle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rayers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RR, RA Haller R.M., Basu A., Baxendale J., Hayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Baxendale J., Hayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Rayer J., Bouck J., Broktein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Rayer J., Dever J., Dietz S.M., RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Fosler C., Gabriellan A.E., Garg N.S., Gelbart M.M., Glasser K., Bourdin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., K. Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin Z., Mays A.D., Dewis P.M., Nelson D.L., Ra Keinston J.R., Pacleb J.M., Pacleb J.M., Pacleb J.M., Pacleb J.M., Pacleb J.M., Ra Merkulvo G., Milshnan N.Y., Mobarry C., Morris J., Moshrefi A., Ra Kimmel B.E., Kodira C.D., Kaft C., Kravitz S., Kulp D., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kaft C., Weisser D.R., Pacleb J.M., Ra Kimmel B.E., Simpon K.A., Nixon K., Sunseri B., Weissen Bach J., Ra Kimmel B.E., Sch
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Best Local
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PROSITE; PS00018; EF-HAND; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 3933 AA; 467876 MW; 5144.
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 FKTEYC-YIVF-----EDTVNKECYY---NVVDGEELD-QEKF----
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(TremBLrel. 13, Last seq
(TremBLrel. 17, Last ann
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Pred. No. :
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368
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. 1e+02;
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Matches 28
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003650;
01-NOV-1996
01-NOV-1996
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EMBL; AY07
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01-JUN-2002
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; He Pterygota; Metazoa; Arthropoda; Tracheata; He Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila. NCBI TaxTha77977
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CG14853.
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                                                         Eukaryota; Euglenozoa;
NCBI_TaxID=5702;
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Stapleton "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome sequence of Drosophila Science 287:2185-2195(2000). EMBL; AE003705; AAR55078-1; -. FlyBase; FBgn0038246; CG14853. SEQUENCE 368 AA; 38008 MW; 2989
        SEQUENCE FROM N.A
                                                                                                                Trypanosoma brucei brucei.
                                                                                                                                                                    Cysteine-rich,
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ch, acidic integral membrane protein p
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tive 21; Mismatches
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THE HUMAN LOW-DENSITY LIPOPROTEIN (LDL), RECEPTOR (PO1130).
-I- CAUTION: CONCERNING THE CONSENSUS SEQUENCE DDCN/DITGDCNET OF
DODECAPEPTIDE REPEATS: UP FROM AA 316 IT IS UNSURE IF IT IS A
ACID N OR D IN POSITION 4 OF THE REPEATS.
EMBL; M55686; AAA30159.1; -.
EMBL; M55686; AAA30170.1; ALT_SEQ.
TIGRFAMS; TIGR01167; LEXTG_anchor; 1.
Membrane; Transmembrane; Antigen; Endocytosis; Signal; Repeat;
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INVOLVED IN RECEPTOR-MEDIATED ENDOCYTOSIS
-i- SUBCELLULAR LOCATION: CELL SURFACE; CONCER
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Lee G.S.M., Bihain B.E., Russell D.G., Deckelbaum R.J., Ploeg L.H.;
"Characterization of a cDNA encoding a cysteine-rich cell surface
protein_located in the flagellar pocket of the protozoan Trypanosom
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Science 282:2012-2018(1998).
EMBL; Z77661; CAB01183.1; ...
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                         EEREDCWTFYANRKYTDFDKSFKK-SSDLDECKKTCFKTEYCYIVFE-----DTVNKE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGDCNETDDCNITGDCNETDDCNITGDCNITGDCNETDDCD 115
                                                                                     EESEDC-----FEKVFLAIISGKHECSK-----DYDFLARNLIQRREALTSGKE
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                                                                                                                                                                                                                                                                                                                                     PF03236;
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Pred. No.
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                                                                                                                                                                                                Mismatches
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Q94648;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2002 (TrEMBLrel. 20,
Cb|AAF22924.1 (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1726
                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by six physically assigned pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyla;eone eudicots; Rosideurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FIW8;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barale J.C., Candelle D., Attal-Bonnefoy G., Dehoux P., Bonnefoy S., Ridley R., Pereira da Silva L., Langsley G., Pereira da Silva L., Langsley G., Pereira da Silva L., Langsley G., Pereira da Reparated "Plasmodium falciparum AARPI, a giant protein containing repeated motifs rich in asparagine and aspartate residues, is associated w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TrEMBLrel. 02, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE FROM N.A.
Yamada K., Banh J., Cha
Lee J.M., Onodera C.S.,
                                                                                                                                                                                                                                                                                                      STRAIN=COLUMBIA;
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SMART; SM00184; RING; 1.
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                                                                                                                                                                                                                                             Nakamura
                                                                                                                                                                                                                                                                   MEDLINE=99087489;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97378065; PubMed=9234746;
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                                                                                                                                                                                                                       Cabata S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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  Chang C.H., Cha
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  Dale J.M., Goldsmith A.D., C., Toriumi M., Wu H.C.,
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Q9FK41;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                              Wwarin J., Schibler U.; "Expression of the liver-enriched transcriptional activator protein DBP follows a stringent circadian rhythm."; Cell 63:1257-1266(1990).
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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MEDLINE-91084854; PubMed-2261643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                          GEELDQE--KFVVDENFTENYLTDCEGKDAGNAAGTGDESDE
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                                                                                                          GEESEEEDRDKDVDPGFRQQLM---EVLQAGNALGGEEEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.
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Similarity to unknown protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                             Hypothetical SEQUENCE 1
                                                                                                                                        PRINTS; PR00507; N12N6MTFRASE.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
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01-MAR-2002
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MEDLINE=98065943; PubMed=9403685;
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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InterPro; IPR002052;
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                                                                                                                                                                                                                                                                                                   rigr; BBH09;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339
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